

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 17:42:00 ; Search time 6486 Seconds
(without alignments)
10932.656 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1636
Sequence: 1 tcacggggctctccgtccg.....aaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb ba.*
- 2: gb hg.*
- 3: gb in.*
- 4: gb om.*
- 5: gb ov.*
- 6: gb pat.*
- 7: gb ph.*
- 8: gb pl.*
- 9: gb pr.*
- 10: gb ro.*
- 11: gb sts.*
- 12: gb sy.*
- 13: gb un.*
- 14: gb vi.*
- 15: em ba.*
- 16: em fun.*
- 17: em hum.*
- 18: em in.*
- 19: em mu.*
- 20: em om.*
- 21: em or.*
- 22: em ov.*
- 23: em pat.*
- 24: em ph.*
- 25: em pl.*
- 26: em ro.*
- 27: em sts.*
- 28: em un.*
- 29: em vi.*
- 30: em hg hum.*
- 31: em hg inv.*
- 32: em hg other.*
- 33: em hg mus.*
- 34: em hg pin.*
- 35: em hg rod.*
- 36: em hg mam.*
- 37: em hg vrt.*
- 38: em sv.*
- 39: em hg hum.*
- 40: em hg mus.*
- 41: em hg other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1275	77.9	1275	6	AX040982	AX040982 Sequence
2	707	43.2	1632	8	AK070211	AK070211 Oryza sat
3	702.2	42.9	1611	8	AB024987	AB024987 Oryza sat
4	497.6	30.4	1043	8	OSCYCOS1	X82035 O.sativa mr
5	402.2	24.6	1777	8	AK070518	AK070518 Oryza sat
6	400.6	24.5	1793	8	OSCYCOS2	X82036 O.sativa mr
7	383.4	23.4	1343	8	MSCYCMS2	X68741 M.sativa cy
8	383.4	23.4	1758	8	MVCYCMS2	X82040 M.sativa mr
9	374	22.9	1706	8	MSCYCMS1	X78504 M.sativa mr
10	372.4	22.8	1700	8	MVCYCMS1	X82039 M.sativa mr
11	364.6	22.3	1999	8	LES243455	AJ243455 Lycopersi
12	357	21.8	1255	6	AX449282	AX449282 Sequence
13	357	21.8	1603	8	ZMU10076	U10076 Zea mays B7
14	357	21.8	1715	6	AX449320	AX449320 Sequence
15	356	21.8	1287	6	AX449286	AX449286 Sequence
16	335.2	20.5	1798	8	ATCYC2B	Z31400 A.thaliana
17	335.2	20.5	1725	8	AK107209	Z31401 A.thaliana
18	249.4	15.2	1725	8	AK107209	AK107209 Oryza sat
19	237.6	14.5	1501	8	ZMU66608	U66608 Zea mays cy
20	234.8	14.4	1632	8	SRCYCB1	Z75660 S.rostrata
21	228.2	13.9	1596	8	GMWYC	X62820 G.max mRNA
22	224.2	13.7	1013	8	AF051225	AF051225 Picea mar
23	223.4	13.7	274	6	AR244904	AR244904 Sequence
24	221.6	13.5	1696	8	LLU24192	U24192 Lupinus lut
25	221.6	13.5	1821	8	PHY250315	AJ250315 Petunia h
26	220.8	13.5	1638	8	NTCYCMRN	Z37978 Nicotiana t
27	220.6	13.5	1659	8	LLU24194	U24194 Lupinus lut
28	218.2	13.3	2373	8	GMWYCLIN	Z26331 G.max Gene
29	216.8	13.3	1597	8	D89635	D89635 Nicotiana t
30	216.2	13.2	954	8	GMWCS37	X62303 G.max mRNA
31	216	13.2	1709	8	D86386	D86386 Catharanthu
32	214.6	13.1	1338	6	AX506094	AX506094 Sequence
33	214.6	13.1	1660	8	ATHCYCIAA	L27223 Arabidopsis
34	211.4	12.9	1345	8	BT006437	BT006437 Arabidops
35	209.4	12.8	1251	8	AK111939	AK111939 Oryza sat
36	207.8	12.7	1490	8	PUMWICY	L34207 Petroselinu
37	206	12.6	1813	8	SOXMCBLTD	D50871 Glycine max
38	205.8	12.6	1782	8	LLU44857	U44857 Lupinus lut
39	205	12.5	2190	8	ZMU66607	U66607 Zea mays cy
40	204.8	12.5	1707	8	TOBNTCYCC	D50737 Nicotiana t
41	203.6	12.4	1600	8	CRGYC1	Y10161 C.rubrum mr
42	203	12.4	1652	8	AMCYCL1	X76122 A.majus cyc
43	202.6	12.4	1251	8	LES243454	AJ243454 Lycopersi
44	197	12.0	1980	6	AX040974	AX040974 Sequence
45	194	11.9	1640	8	AB091346	AB091346 Daucus ca

ALIGNMENTS

RESULT 1
AX040982
LOCUS
DEFINITION Sequence 29 from Patent WO0065040.
ACCESSION AX040982
VERSION AX040982.1 GI:11340578
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Helentjaris T.G., Habben J.E. and Sun Y.
TITLE Cell cycle genes and methods of use

JOURNAL

Patent: WO 0065040-A 29 02-NOV-2000;
PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

Location/Qualifiers

source

1..1275

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

1..1275

/note="unnamed protein product"

/codon_start=1

/protein_id="CAC17048.1"

/db_xref="GI:11340579"

/db_xref="REMBL:CAC17048"

/translation="MAARAADENRRPAAGKPAQVDRDMSARLTDIKLVGAAPYP
AVAKPMLQKSRDKQPALASRRPMTKFAASLAKQGPCQPIVADPEVPCQKE
SYGDTVDIVELVLDGSDSDIDMGATENKIDNDELMDIDSDGPNPLATEY
VKELVTFVRENAKSVRPDYSOODINSKORALIDWL:EVYKFLPMDETPLMV
NLIIDFLEKEVYPRKLOLVGYTAMLLACKVEEVSVPVEDLVISDRYTKGOILEM
EKILINTQFNMSVTPPYVFMKRFKAAADAKQLESLAFMLELCLVYQMLNVRPSH
LAAAVYTAQCAINRCQHWTKVCEHSRYTSDLLECSRMMVDFHQKAGTSKLTGVHR
KISTYKFCGVAKILPAQFLLESGETPPPSGAN"

ORIGIN

Query Match 77.9%; Score 1275; DB 6; Length 1275;

Best Local Similarity 100.0%; Pred. No. 6.8e-299;

Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY : 109 ATGGCGCGCGCGCGCTGACGAGAACAGGAGACCGGCGGAGGAGCCCGCCGACGCG 168
Db : 1 ATGGCGCGCGCGCGCTGACGAGAACAGGAGACCGGCGGAGGAGCCCGCCGACGCG 60
QY : 169 GTCGAGACATGCGGAGCGCGCGCTGACGAGACATCAAGAACCTCTCGCGGCTGCC 228
Db : 61 GTCGAGACATGCGGAGCGCGCGCTGACGAGACATCAAGAACCTCTCGCGGCTGCC 120
QY : 229 CCCTACCCCTACGCGCTGCGCAAGAACCCATCTCCAGAGAGCAAAAGGAGCAAG 288
Db : 121 CCCTACCCCTACGCGCTGCGCAAGAACCCATCTCCAGAGAGCAAAAGGAGCAAG 180
QY : 289 CAGCCAGCGTTGCAAGCAGCGCGCGCTGACGAGAAATTCGCGCCCTCTTGGCGAGC 348
Db : 181 CAGCCAGCGTTGCAAGCAGCGCGCGCTGACGAGAAATTCGCGCCCTCTTGGCGAGC 240
QY : 349 AAGGGCCAACTCAAGTGTACGCGATGCTAGCTGATCCAGAACCCGAACTTTGTCAACAG 408
Db : 241 AAGGGCCAACTCAAGTGTACGCGATGCTAGCTGATCCAGAACCCGAACTTTGTCAACAG 300
QY : 409 AAGGAATCAGTAGCGGATGCCACGTTGATATTGACGTGAATCTACGAGCTGCTCGAC 468
Db : 301 AAGGAATCAGTAGCGGATGCCACGTTGATATTGACGTGAATCTACGAGCTGCTCGAC 360
QY : 469 GGTAGTCATAGTACATCGACATGGGTGCGACAGAAACAAAGGACATTTATGAACGAAGAT 528
Db : 361 GGTAGTCATAGTACATCGACATGGGTGCGACAGAAACAAAGGACATTTATGAACGAAGAT 420
QY : 529 GAATGTCTCATGATATTGACATGTCAGATCGCGGAAACCCGTTGCTGCAACAGATAT 588
Db : 421 GAATGTCTCATGATATTGACATGTCAGATCGCGGAAACCCGTTGCTGCAACAGATAT 480
QY : 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAAGCCAGAT 648
Db : 481 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAAGCCAGAT 540
QY : 649 TACATGTCAGCCCAACAGACATAAATCAAGATGAGAGCAATCTGTAGTACTGCTG 708
Db : 541 TACATGTCAGCCCAACAGACATAAATCAAGATGAGAGCAATCTGTAGTACTGCTG 600
QY : 709 ATTGAGGTTCACTACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 768
Db : 601 ATTGAGGTTCACTACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 660
QY : 769 ATAGATAGATTTTGGAAAAAGGAGTGCTTCCAAAGGAGGAGCTACAACTGGTTGGAGTC 828
Db : 769 ATAGATAGATTTTGGAAAAAGGAGTGCTTCCAAAGGAGGAGCTACAACTGGTTGGAGTC 828
```

```
Db 661 ATAGATAGATTTCTTGAAAAAGGAGTGCTTCCAAAGGAGGAGCTACAACTGGTTGGAGTC 720
QY 829 ACAGCTATGCTGCTGCTTTGTAATAATAGAGAGGTATCTGTTCCAGTCTTTGAGGACCTT 888
Db 721 ACAGCTATGCTGCTGCTTTGTAATAATAGAGAGGTATCTGTTCCAGTCTTTGAGGACCTT 780
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGCGCAATTTTGAATATGGAAGTGTGATT 948
Db 781 GTGCTGATATCTGACCGTGCCTACACAAAGGCGCAATTTTGAATATGGAAGTGTGATT 840
QY 949 CTGAACACGCTGCAGTTCAACATGCTGTTTCCAAACACCTTATGTTCTTCTATGAAGAGTTT 1008
Db 841 CTGAACACGCTGCAGTTCAACATGCTGTTTCCAAACACCTTATGTTCTTCTATGAAGAGTTT 900
QY 1009 CTGAAGCTGCAGATCGAGATTAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTC 1068
Db 901 CTGAAGCTGCAGATCGAGATTAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTC 960
QY 1069 TGCTTGTAAGATACCAATGCTGAATATCGGCTTCGATCTGCTGCTGCTGCTGCTGCTGCT 1128
Db 961 TGCTTGTAAGATACCAATGCTGAATATCGGCTTCGATCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1129 TATAGTCACAGTGTGCTATCAATCGTTGCGAGCACTGCAAAAGCTCTGCGAGCTCTCAT 1188
Db 1021 TATAGTCACAGTGTGCTATCAATCGTTGCGAGCACTGCAAAAGCTCTGCGAGCTCTCAT 1080
QY 1189 AGCAGATACACTAGCGACCAACTCTCGGAGTGTCTCGAGGATGATGTTTTCACCCAG 1248
Db 1081 AGCAGATACACTAGCGACCAACTCTCGGAGTGTCTCGAGGATGATGTTTTCACCCAG 1140
QY 1249 AAGCTGGAACCACTAGCTCACTGCGGTGCACAGAGTACAGTACCTACAGTTCGCT 1308
Db 1141 AAGCTGGAACCACTAGCTCACTGCGGTGCACAGAGTACAGTACCTACAGTTCGCT 1200
QY 1309 TCGTGCCCAAGATTTTTCCTGCGGCTGCTGCTGCGAGTCCGAGGAGCAACCGCTCTCT 1368
Db 1201 TCGTGCCCAAGATTTTTCCTGCGGCTGCTGCTGCGAGTCCGAGGAGCAACCGCTCTCT 1260
QY 1369 TCAGGTGCAAACTAG 1383
Db 1361 TCAGGTGCAAACTAG 1275
```

RESULT 2

AK070211

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AK070211 1632 bp mRNA linear. PLN 24-JUN-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J023043123, full
insert sequence.
AK070211 GI:32980235
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Hotta, I.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Teunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, J., Carrinci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Otsu, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,

Yoshino,M. and Hayashizaki,Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

Science 301 (5631), 376-379 (2003)

22752273

1269764

2 (bases 1 to 1632)

Adachi,J., Aizawa,S., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayashizaki,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,Y., Ikeda,R., Imamura,K., Inotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kawagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Nariikawa,R., Niikura,J., Nishi,K., Nomura,K., Nunakaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Ootani,N., Oka,Y., Ootani,Y., Ryo,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

Direct Submission

TITLE

JOURNAL

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,

Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica

rice.

URL : <http://cdna01.dna.affrc.go.jp/cdna/>

NRAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Otono,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Nariikawa,R., Niikura,J., Oka,M., Ryo,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ootani,N., Oka,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

Location/Qualifiers

1. 1632

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="J023043123"

ORIGIN

Query Match

Best Local Similarity

43.2%; Score 707; DB 8; Length 1632;

73.5%; Pred. No. 9.5e-161;

	Matches	968;	Conservative	0;	Mismatches	320;	Indels	29;	Gaps	4;
QY	114	GGCGGGCGGCTGACGAGAACGAGACCGCGCGCGAGGAGCCCGCGCGAGGAGCCCGCGCGAGGAGCCCG	173							
DB	89	GGATAGGCGGAGGAGAACCGGAGGCTGGCGCGGCTGGCGGAGGAGCCCGCGCGAGGAGCCCG	148							
QY	174	AGACATGCGGAGCGGCGGCTCAACGACATCAAGAACCTCGTCGCGGCTGCGGCGGCTGCGGCGGCTG	233							
DB	149	AGAGATGGGAAACCGGAGGCGGCTCAGGACATCAACAACTCGTCGCGGCGGCGGCGGCGGCTG	208							
QY	234	CCCTTACCGCTCCCGAGAGCCATCTCGACGAGGAGCAAAAGGAGCAAAAGGAGCAAAAGGAGCAAA	293							
DB	209	CCGCTCCCGGATCGGCAAGAACCGGATCTAGAGAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGG	268							
QY	294	AGC---GTTGGCAAGCAGCCCGCCCATCAACAAAGGAAATTCGCCCGCTCTCTTTGGGAGGAGCA	350							
DB	269	TGCAATTGGTGGTGGAGCCACCGGCTATGACGAGGAAATTTTCGCGGCTCTCTTTGACCGGAGAA	328							
QY	351	GGGCAACCTGATGTGACGCGATCTAGCTGATCCAGAACCCG---AGTTTGTCAACA	407							
DB	329	AGAACAGGCTTGACCATCAGGTTTCGCTGGCTGATGACGCGGCTGCTGTCATCTGATCCACA	388							
QY	408	GAAGGAATCAGTAGCGATGGCACCGTTGATATTGACGTGAACTCTACGAGCTGGTGA	467							
DB	389	GAAGAACCCATCCCGATGGCACAGTTGACGACGATGTGGAATCGTGCAGATCGAACGA	448							
QY	468	CGTGTGATGTGATCATGTCATCGGCTGCGACGAGAACGAGACATTTGAAAGGAGAA	527							
DB	449	CTATA-----TTGCGTGGATGATGCAATGATCTGATGAGGA	487							
QY	528	TCAATTGCTCATGGATATTGACGTGACAGCTCGGGAACCCGCTTGCTGCTCAACAGAAATA	587							
DB	488	TGAGTCCATGATGACATTTGACGTGCGGCTCAGGAAATCCGCTTCGACGACCGAGTA	547							
QY	588	TGTTAAAGAGCTTTACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAGGCGCAGA	647							
DB	548	CGTCAGAGTTGTCAAGTTCTATAGAGAAATGAGGAAATGAGTTGTGTGCGAGCCTGA	607							
QY	648	TTACATGTCACGACCAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATTTGATGGCT	707							
DB	608	TTACATGTCAGTCAAGGACATTAATGAAGAATGAGCAATTTCTGATTTGATGGCT	667							
QY	708	GATTGAGTTCACTCAAGTTTGAATGATGATGAGAGCGCTCTTTCTTTATGTTAAACAT	767							
DB	668	CATTGAGTCCATCACAAGTTTGGCTGATGATGAGAGACTCTCTTTCTTACTGTTAAACAT	727							
QY	768	AATGATGATTTCTTGGAAAGGAGTGGTTCCAGGAGAGAGCTACACTGTTGAGT	827							
DB	728	AGTAGAGATTCTTGGAAAGGAGTGGTTCCAGGAGAGAGTGGCTGAGTGGAGT	787							
QY	828	CACAGCTATGCTGCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCT	887							
DB	788	GACAGCTATGCTCTCTTGTGTTCAATATGAGGAGTGGCAGTCCCTGCTGCGAGGATCT	847							
QY	888	TGTGCTGATATCTGACCGCTGCTACACAAAGGCAATTTAGAAATGGAAGAGTTCAT	947							
DB	848	AGTGCTAATTTCTGACCGGCTTATACAAAGGCAAGTCTCGAAATGGAAGAGTTCAT	907							
QY	948	TCTGAACACGCTGAGTTTCAACATGCTGTTTCCAAACACCTTATGCTCTCATGAAGAGGTT	1007							
DB	908	CCTAAACACACTCCAGTTTCAACATGCTGTGTACCAACACCTTTACGTTTTTATGAGACGTT	967							
QY	1008	TCTGAAGCTGCAGATGACAGTAAACAGCTTGAGCTAGCTAGCTATTTTCATGCTGGAGCT	1067							
DB	968	TCTGAAGGACCTCAGTCTGCAAGAGCTACAGCTACTTTCTCTTTTCATCTTGGAGCT	1027							
QY	1068	CTGCTTGTGAGATACCAATTCGTAATTTATCGGCTTCGATCTGGCTGCTGCTGGGCT	1127							
DB	1028	CTCCCTGGTGGATACCAATGCTCAAGTACCGACCTTCGCTTCTTCTGCTGCTGAGT	1087							
QY	1128	TTATCTGCAAGTGTGCTATCAATCGTTGCCAGCACTGACAAAGTCTTCGAGTCTCA	1187							
DB	1088	TTACACAGCAATGTGCTCTCACTCGTTGCCAGCTGGACAAAGACCTTCGGAATACA	1147							


```

QY 1188 TAGCAGATACACTAGCGACCAACTCTCTGGAGTCTCGAGATGATGGTAGATTTTCAACA 1247
Db 1135 TAGTAGATATACCGGAGAGCAGCTTCTTGAGTGTCTTAGGATGATGGTAGATTTCCACCA 1194
QY 1248 GAAGGCTGGAACAGTAAGCTCACTGCGTGCACAGGAAGTACAGTACCTACAAAGTTGG 1307
Db 1195 GAAGGCGGAGCAGGACAGCTCACCGCGGTGCACCGGAATACAGTACGTTCAAGTTGG 1254
QY 1308 TTCCGTTGGCAAGATTTTTCCTCGGAGTTCTCTGCTGGAGTGGGAG--GGACACGGCT 1365
Db 1255 GTGTGACGCAAAACGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1314
QY 1366 CTTTCAGGTGCAACTAGTGTGATCGACCTATTCACTGGTGGATTTTAAAGTT 1422
Db 1315 CTTTCAGAGCAGCCTGTGTAAGTAATCTATTTCCCTCGATAGATTTTAACTT 1371

RESULT 4
LOCUS OSCYCOS1 1043 bp mRNA linear PLN 26-NOV-1996
DEFINITION O.sativa mRNA for cyclin 1.
ACCESSION X82035
VERSION X82035.1 GI:558620
KEYWORDS cyclin; cycos1 gene.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS Sauter, M., Mekhedov, S.L. and Kende, H.
TITLE Gibberellin promotes histone H1 kinase activity and the expression
of cdc2 and cyclin genes during the induction of rapid growth in
deepwater rice internodes
JOURNAL Plant J. 7 (4), 623-632 (1995)
MEDLINE 95261415
PUBMED 7742859
REFERENCE 2 (bases 1 to 1043)
AUTHORS Kende, H.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1994) H. Kende, MSU-DOE Plant Research
Laboratory, Michigan State University, East Lansing, MI 48824-1312,
USA

FEATURES
source Location/Qualifiers
1..1043
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/tissue_type="internode sections"
/clone_lib="lambda ZAPII cDNA"
/dev_stage="mature plant"
1..1043
/gene="cycos1"
<1..731
/gene="cycos1"
/codon_start=3
/product="cyclin"
/protein_id="CAAS7555.1"
/db_xref="GI:558621"
/db_xref="GOA:Q40670"
/db_xref="SPRMBL:Q40670"
/translation="OQDINEMRAILDLIEVHKFELMDETLFTLVNIVDFLEKQ
VWPKLILGVMTAMLLACKVEVAVPVVDELVLISDRVTKGQILEMEKILINTLQF
NMSVPTIYVFRFLKAAQSDKQLILSFILSELVVEOMLYKRSLLSAAAVYTAQ
CALTRCQWTKTICLHRYTGEQLLECSRMVDFHQVAGAGKLTGVHRYKYSTFKFCA
AKTEPAFLLESAGGYNLKKQC"

gene
CDS
Query Match 30.4%; Score 497.6; DB 8; Length 1043;
Best Local Similarity 79.0%; Pred. No. 7.2e-110;
Matches 605; Conservative 0; Mismatches 159; Indels 2; Gaps 1;

ORIGIN
659 GCCAACAGACATAACTCAAGATGAGACGAATCTTGATTGACTGCTGCTGATGAGGTTTC 718

```

```

Db 1 GTCAAGGAGACATAAAATGAAAAGATGAGAGCAATTCGTGATGATGGCTCATGGAGTCC 60
QY 719 ACTACAAAGTTTGAACCTGATGATGAGACGCTCTTTCTTATGTTGTTAAACATAATAGATAGAT 778
Db 61 ATCAAAATTTGAGCTGATGATGAGACTCTCTTTCTTACTGTTTAAACATAGTAGACAGAT 120
QY 779 TCTTGGAAAGGAGTGGTTCCAAAGGAAGCTACAACTGTTGGTGGAGTCAACAGCTATGC 838
Db 121 TCTTGGAAAAACAAGTTGTGCCAAGGAAGAGTTGCGAGCTAGTTGGAGTAGACACTATGC 180
QY 839 TGCTCGCTTGTAAATATGAGGAGGTATCTGTTCAGTGTGTTGAGGACCTTGTGCTGATAT 898
Db 181 TCCTTGCTTGCANATATGAGGAGTCCAGTCCCTGTCGTCAGGATCTAGTGTCTAATTT 240
QY 899 CTGACCGTGCCTACACAAAAGGGCAAAATTTAGAAATGGAAAGTTGATTTCTGACACGC 958
Db 241 CTGACCGGGCTTATACAAAAGGCAAAATTTCTGAAATGGAAAGTTGATCTTAAACACAC 300
QY 959 TGCAGTTCAACATGCTGTGTTCCAAACACCTTATGTCCTCATGAAGAGGCTTTCTGAAAGCTG 1018
Db 301 TCGAGTTCAACATGCTGTACCAACACCTTACGTTTATGAGACGCTTTCTGAAGGCAG 360
QY 1019 CAGATGCAGATAAACAGCTTGAGCTAGCTGCTCAATTTTTCATGCTGGAGCTCTGCTGTAG 1078
Db 361 CTCAGTCTGACAAGCAGCTACAGCTACTTTCTCTTTTCACTCTGAGCTCTCCCTGTGG 420
QY 1079 AATACCAAACTGCTCAATTTATCGGCTTCGCACTCTGGCTGCTGCTGCGGTTTATACTGCAC 1138
Db 421 AATACCAAACTGCTCAAGTACCGACCTTCGCTCTCTCTGCTGCTGAGTTTACACAGCAC 480
QY 1139 AGTGTGCTATCAATCGTTGCCAGCACTGGACAAAGGCTCTGGAGTCTCATAGCAGATACA 1198
Db 481 AATGTGCTCTCACTCGTTGCCAGCAGTGGACAAAGACCTGCGAACTACATAGTAGATATA 540
QY 1199 CTAGCGACCAACTCTCTGAGTCTCGAGGATGATGTTAGTATTTTACCAGAAAGCTCGAA 1258
Db 541 CGGAGAGCAGCTTCTTGAGTCTTAGATGATGTTAGATTTCCACAGAAAGGCCGAG 600
QY 1259 CCAGTAAGTCACTGGGCTGCACAGGAAGTACACTACTACAAGTTCGTTGCTGGTGGCCA 1318
Db 601 CAGGCAAGCTCACCGGCTGCACCGGAATACAGTACGTTCAAGTTTGGTGTGCGAGCCA 660
QY 1319 AGATTTTCCCTGCGCAGTTCCTGCTGGAGTCGGAG--GGACACCGCTCTCTCAGGTGC 1376
Db 661 AAACGAGCCTGCTCTCTCTTGTGTTGAGTCAGGAGGAGGTTTACACCTTAGAAGC 720
QY 1377 AAACTAGTGAATCGACCTATTCAACTGGTGGATTTTAAAGTT 1422
Db 721 AGCCTTGTGATGAATCAATCTATTCCTGATAGATTTTTTAACTT 766

RESULT 5
AK070518 1777 bp mRNA linear PLN 24-JUL-2003
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:J023055K12, full
DEFINITION insert sequence.
ACCESSION AK070518
VERSION AK070518.1 GI:32980542
KEYWORDS FLI cDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Teshikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Otomo, Y., Murakami, K.,

```


TITLE Alfalfa cyclins: differential expression during the cell cycle and in plant organs
JOURNAL Plant Cell 4 (12), 1531-1538 (1992)
MEDLINE 93104677
PUBMED 1307238
REFERENCE 2 (bases 1 to 1343)
AUTHORS Hirt,H.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1992) H. Hirt, Inst of Microbiology, Univ of Vienna, Biocenter, Dr Bohrgasse 9, 1030 Vienna, AUSTRIA
FEATURES
source
1..1343
/organism="Medicago sativa"
/mol_type="mRNA"
/db_xref="taxon:3879"
1..1343
/gene="CYCMS2"
/genes="CYCMS2"
/notes="Cyclin homolog of B type. Cyclin B is associated with CDC2 kinase and regulates entry and exit into and from mitosis"
/codon_start=1
/product="cyclin"
/protein_id="CAA48675.1"
/db_xref="GI:19599"
/db_xref="GOA:P30278"
/translation="NSNERGFIADIDDELKLPEDPEPMTLEHPHSDPLEMEVEE MEDIEGMLIDISCDANNLAVYIEDLHAYRKIYLGCVSPTYMDEOLDLNEBM RALLDGLLVHDKEDPLMOETPLTNLIDFLAKONVVRKQLQGLVAMLLACKYE EUSVPVYDLIHIDRANVTRKDLSEKMLMNTLOYNSLPTAVFVRFLKAAQARK KLELVAFFLDLSVEYEMKFPFSLVAAAAYITACQTSVGFKNWKTCEWHNTYSED QLLDECSNLMVGFHQKAGAGKLTGVHRKYGSAKFSPTACEFACFLEENKQNP"
ORIGIN
Query Match 23.4%; Score 383.4; DB 8; Length 1343;
Best Local Similarity 66.5%; Pred. No. 4.5e-82;
Matches 549; Conservative 0; Mismatches 276; Indels 0; Gaps 0;
Qy 523 GAAGATGAATGCTCATGATATGACAGTCAGAGCTCGGGAAACCCGCTGCTCAACA 582
Db 145 GAGGAGAGATGATTTGGACATGATGATGATGATGATGATGATGATGATGATGAT 204
Qy 583 GAATATGTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAG 642
Db 205 GAGTATATGAAGATCCATGCTTACTACAGAAAGATGATGATGATGATGATGATGAT 264
Qy 643 CCAGATACATGTCACCAACAGACATAACTCAAGATGAGAGCATTTCTGATTGAC 702
Db 265 CCAACCTACATGATGAACAACTTGACCTCAATGAGAGGATGAGGCTATACATGATGAC 324
Qy 703 TGGCTGATGAGGTTCACTACAAAGTTTGAACCTGATGATGAGACGCTCTTTCTTATGTA 762
Db 325 TGGCTGATGAGGTTCACTACAAAGTTTGAACCTGATGATGAGACGCTCTTTCTTACAT 384
Qy 763 AACATATAGATAGTCTTGGAAAGGAGTGGTCCAGAGGAGAGCTCAACCTGCT 822
Db 385 AATCTATCAGACATTTCTGGCTAGCAGATGTTGTAGAGAAATCTCAGCTGTT 444
Qy 823 GAGATCAGATATGCTGCTCGTTGTGTAATATGAGAGGATATCTGTTCCAGTTTGTAG 882
Db 445 GGTCTGTTGCCATGCTTTTGGCATGCAAGTATGAGAGGATTTCTGTGCTGCTGTTTCG 504
Qy 883 GACCTTGTGTATCTGACCTGCTCTACACAAAGGGCAATTTTGAATGAAAG 942
Db 505 GATCTGATCATATAGCTGACAGCTTACACAGGAAGACATTTTGAATGAGAG 564
Qy 943 TTGATTCGACAGCTGCAAGTTCACATGCTGTTTCCAAACCTTATGCTTTCATGAG 1002
Db 565 TTGATGCTCAACATCTGCAAGTATACATGCTCTTCCAACTGCTTATGTTTTCATGAG 624
Qy 1003 AGGTTTCTGAAGCTGCAGATGCAGATAAACAGCTTGAGTACGCTCATTTTTCATGCTG 1062

Db 625 AGGTTTCTGAAGGCTGCTCAAGCTGCACAAAAAAGCTTGAAGCTGGTGGCTTTTCTTGGTT 684
Qy 1063 GAGCTCTCTGTTAGATACCAAAATGTAATATCGGCTTCGCAATCTGGTGTGCTGCT 1122
Db 685 GACCTATCTCTGGTGAATATGAGATGCTGAAGTTTCCACCATCTTGGTGTGCTGCT 744
Qy 1123 GCGGTTTATCTGACAGCTGCTTCAATCGTTGCGAGCACTGGACAAAGGCTGCGAG 1182
Db 745 GCTGCTTACAGCTCAATGCACTGCTGAGTGTTCAAACACTGGAACAAGACATGTGAG 804
Qy 1183 TCTCATAGCAGATACACTAGCGACCAACTCCTGAGTGTCTCGAGGATGATGATGATTT 1242
Db 805 TGGCACACAAACTACTCAGAAGATCAGCTGTTGAGTGTCTATGCTGATGTTGGATT 864
Qy 1243 CACAGAGGCTGGACCAAGTAAGCTCAGTGGCTGCACAGGAGTACAGTACTACAG 1302
Db 865 CACCAGAAAGCCGAGCGGAGAACTGACAGGATGATAGGAGTATGGCTAGCAAAA 924
Qy 1303 TTGCGTTGCTGGCCCAAGATTTTGCCTGCGCAGTCTCTGCTGGAG 1347
Db 925 TTAGCTTCACTGCTAAATGTGAACACAGCATGTTTCTTCTGGAG 969

RESULT 8
MVCYMS2 1758 bp mRNA linear PLN 19-JUL-1995
LOCUS M varia mRNA for mitotic cyclin 2.
DEFINITION X82040
ACCESSION X82040
VERSION X82040.1 GI:914862
KEYWORDS CYCMS2 gene.
SOURCE Medicago sativa subsp. x varia
ORGANISM Medicago sativa subsp. x varia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 1758)
AUTHORS Meskine,I., Bogre,L., Dahl,M., Pirck,M., Ha,D.T., Swoboda,I.,
Heberle-Bors,E., Ammerer,G. and Hirt,H.
TITLE cycms3 a novel B-type alfalfa cyclin gene, is induced in the
JOURNAL G0-to-G1 transition of the cell cycle
MEDLINE 95375541
PUBMED 7647566
REFERENCE 2 (bases 1 to 1758)
AUTHORS Pirck,M.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1994) M. Pirck, Inst for Microbiology & Genetics,
University of Vienna, Dr. Bohrg. 9, 1030 Vienna, AUSTRIA
COMMENT Related sequences: X68740, X68741, S53351 and S53352.
FEATURES
source
1..1758
/organism="Medicago sativa subsp. x varia"
/mol_type="mRNA"
/sub_species="A2"
/db_xref="taxon:36902"
1..1758
/gene="cycms2"
98..1402
/gene="cycms2"
/codon_start=1
/protein_id="CAA57560.1"
/db_xref="GI:914863"
/db_xref="GOA:P46278"
/translation="MVNTSENNNAVMPKFGGMMQVGHGGRIYVGNRALGGIN
QNFVGRFPYCVVHKVLSERKEICEKQADLGRPTIRFPAKIASQSQSYAKTKN
SDPLNLFNSIAIDDELKSPEDPEPMTLEHPHSDPLEMEVEEVEDISEMIL
NIDSCDANNLAVYIEDLHAYRKIEYLGCVSPTYMDEOLDLNEBMRAILLVDMLIS
VDFDPLAQETLFTLIDFLAKONVVRKQLQGLVAMLLACKYEVSVPVYDL
IHIDRANVTRKDLSEKMLMNTLOYNSLPTAVFVRFLKAAQARKLELVAFFLV
DLSLVEYEMKFPFSLVAAAAYITACQTSVGFKNWKTCEWHNTYSEDQLLECSMLAV

KEYWORDS	cyc gene; cyclin.
SOURCE	Medicago sativa
ORGANISM	Medicago sativa
REFERENCE	1 Savoure, A., Feher, A., Kalo, P., Petrovics, G., Csanadi, G., Szecsi, J., Kiss, G., Brown, S., Kondorosi, A. and Kondorosi, E. Isolation of a full-length mitotic cyclin cDNA clone CycIIIMs from Medicago sativa: chromosomal mapping and expression Plant Mol. Biol. 27 (6), 1059-1070 (1995) 7766889
AUTHORS	Savoure, A.
TITLE	Direct Submision
JOURNAL	Submitted (29-MAR-1994) A. Savoure, CNRS, Institut des Sciences Vegetales, Avenue de la Terrasse, 91198 Gif-Sur-Yvette Cedex, FRANCE
MEDLINE	7766889
PUBMED	7766889
REFERENCE	2 (bases 1 to 1706)
AUTHORS	Savoure, A.
TITLE	Direct Submision
JOURNAL	Submitted (29-MAR-1994) A. Savoure, CNRS, Institut des Sciences Vegetales, Avenue de la Terrasse, 91198 Gif-Sur-Yvette Cedex, FRANCE
FEATURES	Location/Qualifiers
source	1..1706
	/organism="Medicago sativa"
	/mol_type="mRNA"
	/sub_species="varia"
	/db_xref="taxon:3979"
	/clone="AS9D"
	/haplotype="tetraploid"
	/tissue_type="young nodules"
	/clone_lib="lambda ZAP II"
gene	1..1706
	/gene="CycIIIMs"
CDS	137..1423
	/gene="CycIIIMs"
	/note="close homolog of CycMs1 and CycMs2 B-like cyclin"
	/codon_start=1
	/product="B-like cyclin"
	/protein_id="CAA5272.1"
	/db_xref="GI:780267"
	/db_xref="GOA:Q40337"
	/db_xref="SPTREMBL:Q40337"
	/translation="MKTSEENNVPNTPEGLDSRKVGONRRALGVINONLVGEKPYCVNKGALSERNDVCEKQADVPVRLPITRFAAKIANTKTINAGTTKRSNLAKS SNGDPLFIYVDDEHKVEDQVPMALKEQEPHMSDESDRMEVEVEMEDIMPEVMDIT PDANDPLVASYIEDLYSYRKYKSCVSPFNQAQFDINERMARLLVNLWLEHVDK FDLMEETFLVNLNIDFLKQSVVRKKGLGVMLLACKYEEVSPVVPVVDLILIS DRATRKLEVMKVMNLFENI SVPTAYVVRERFLKQAADRKLFLFLLELS VEYAMLKPSQLAAAVYTAQTMVGVKQMSKTCWEHTNYSEDQLLECSLMVDFPKH KAGTGKLTGAHRKYCTSKFSYTAKECPASFLLENEL"
ORIGIN	
Query Match	22.9%; Score 374; DB 8; Length 1706;
Best Local Similarity	65.9%; Fred. No. 9.1e-80;
Matches	542; Conservative 0; Mismatches 280; Indels 0; Gaps 0;
QY	526 GATGAATTGCTCATGGATATTGACAGTCGACAGCTCGGGAACCCGCTTGTGCAACGAA 585
DB	590 GAAGACCTGTTATGACATTGACACCCCTGATGCAATGACCTCTTGACGTTGCTGAA 649
QY	586 TATGTTAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAGAGCTGTGTGAAGCCA 645
DB	650 TATATCGAAGATCTTTACTCTTACTACAGAAAGTTGAGAGTACTAGCTGTGTTTCA 709
QY	646 GATTACATGTCGAGCAACAGACATAAAGCTCAAGATGAGAGCAATTCGATTGACTGG 705
DB	710 AACTATATGGACAGCAATTTGACATTATGAAGAGATGAGAGTACTACTGTTGACTGG 769
QY	706 CTGATTGAGGTTCACTACAGTTTGAAGTGTGATGATGAGCGCTCTTCTTATCGTAAAC 765
DB	770 CTATTGAGGTCATGACAAATTCGACCTCATGATGAGACATTTCTTCTCAGTGTCAAT 829
QY	766 ATAATAGATAGATTCTTGGAAAGGAAGTGTGTTCAAGGAAGAAGCTACAACTGGTGA 825

Db 830 CTTATAGACAGATTTTGGAAAGCAGTCTGTGTGAAGAAAGCTTCAGTTGGTTGT 889
 QY 826 GTACAGAGTATGCTGCTGTGTAATATGAGAGAGTATCTGTCCAGTTGTGAGGAC 885
 Db 890 CTAGTGGCAATGCTTTGGCAGTCAAGTATGAGGAAGTTTCAGTGCCCTGGTGGAGAT 949
 QY 886 CTTGCTGTATATCTGACCGTCTTACACAAAAGGGCAAAATTTTGAAGATGAAAAGTTG 945
 Db 950 CTAATCTTATATACAGACAGACATACACCCGGAAGAGAGTTCTGGAATGGAAGGTG 1009
 QY 946 ATTCTGAACAGCTCAGTTCAACATGCTCTTCCACACCTATGCTTCTCATGAAGAG 1005
 Db 1010 ATGTAATGATTTGAAGTTTAAATATCTGTGCAACAGCCTAAGTTTTCATGAAGG 1069
 QY 1006 TTTCTGAAGCTGAGATGAGATAAAGAGCTTGTGAGTGTAGTCTTTCATGCTGGAG 1065
 Db 1070 TTTCTGAAGGGGGCTCAAGACAGACAGAAAACCTTGAGCTGTAGCTTTCTTCTGATTGAG 1129
 QY 1066 CTTCTGCTTGGTAGAATACAAATGCTGAATTTATCGGCTTTCGATCTGGCTGCTGCG 1125
 Db 1130 CTATCTCTGTAGAAATAGCAATGTTGAAGTTCTCTCTCTCACTAGTGTGCGTGT 1189
 QY 1126 GTTATATGACAGTGTGCTATCAATCGTTGCGAGCAGTGTGCAAGAGTCTCGAGTCT 1185
 Db 1190 GTCTATACAGCTCAATGACCTATGTATGGTGTCAACAGTGTGAGTGAATGG 1249
 QY 1186 CATAGACATACACTAGGACCAACTCTGAGTGTGCGAGGATGATGGTAGATTTTCAC 1245
 Db 1250 CACACCACTACTCTGAGATCACTCTTAGAATGCTCTAGTTTATGTTGATTTTCAC 1309
 QY 1246 CAGAAGGTGGAACAGTAAGTCACTGCTGGGTGCGACAGGAAGTACAGTACCTACAGTTC 1305
 Db 1310 AAGAAGGTGGGACAGGAAACTTACAGAGGACATAGGAAGTATTGCATCAAAATTT 1369
 QY 1306 GTTCTGCTGGCAAGATTTTGGCTGCGCAGTTCTGCTGCGAG 1347
 Db 1370 AGCTATCTGCGAAATGTGACACAGCAAGTTTCTTCTGCGAG 1411

RESULT 10

MVCYCMS1
 LOCUS M.varia mRNA for mitotic cyclin 1. 1700 bp mRNA linear PLN 19-JUL-1995
 DEFINITION X82039
 ACCESSION X82039
 VERSION X82039.1 GI:914860
 KEYWORDS cymc1 gene
 SOURCE Medicago sativa subsp. x varia
 ORGANISM Medicago sativa subsp. x varia
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 REFERENCE 1 Mesikene, I., Bogue, L., Dahl, M., Pirck, M., Ha, D.T., Swoboda, I.,
 Heberle-Bors, E., Amerer, G. and Hirt, H.
 Cymc3, a novel 3-type alfalfa cyclin gene, is induced in the
 G0-to-G1 transition of the cell cycle
 Plant Cell 7 (6), 759-771 (1995)
 JOURNAL MEDLINE
 PUBLISHED 95375541
 REFERENCE 2 (bases 1 to 1700)
 7647566
 AUTHORS Pirck, M.
 TITLE Direct Submission
 JOURNAL Submitted (04-OCT-1994) M. Pirck, Inst for Microbiology & Genetics,
 University of Vienna, Dr. Bohr, 9, 1030 Vienna, AUSTRIA
 COMMENT Related sequences: X68740, X68741, S53351 and S53352. Related
 sequences: X68740, X68741, S53351 and S53352.
 LOCATION/Qualifiers
 1. 1700
 /organism="Medicago sativa subsp. x varia"
 /mol_type="mRNA"
 /sub_species="A2"

gene /db xref="taxon:36902"
 1..1700
 CDS /gene="cymc1"
 133..1419
 /gene="cymc1"
 /codon_start=1
 /protein_id="CAA57559.1"
 /db xref="GI:914861"
 /db xref="GOA:P46277"
 /db xref="SWISS-PROT:P46277"
 /translation="MKFSSEKVNPNPTNFEGLDSRKVGNRGLVGNLNVVEGR
 PYCVNKRALSERNVCEKQKQADPVHRPITRRPAKIASTKTSNAGVTIKRNLAKS
 SNGFGDIFVDDHEPVEDQVPVMALEQTEPMHSESDMEVEEMEDMEPVEDIDT
 PDNDPLAIEYIEDIYSYRKVESVCSVPNYNAQQDINERMAIIVLWLEIYVHDX
 FDMHETLFJTNLIDRFLEKQSVVRKKQLVGLVAMLLACKYEEVSVVVGDLILIS
 DRAITKEVLEMEKVMNALKFNISVPTAYVFMRFKFAAQAADRLKLELLAFLBLSL
 VETAMLKFSPLAAAVTAQCTMYGVKQMSKTCMEWHTNYSQDQLLECSLWVDFHX
 KAGTGKLTGAHRKYCTSKFSYAKCEPASFILENEL"
 misc_feature 220..246
 /gene="cymc1"
 /note="destruction box"
 ORIGIN
 Query Match 22.8%; Score 372.4; DB 8; Length 1700;
 Best Local Similarity 65.8%; Pred. No. 2.2e-79;
 Matches 541; Conservative 0; Mismatches 281; Indels 0; Gaps 0;
 QY 526 GATGAATGCTCATGATATGACGTGACAGTCCGGGAAACCCGCTGCTCAACAGAA 585
 Db 586 GAAGAGCCTTTATGACATTTGACCCCTGATGCAATGACCCCTCTTGCAGTTGTA 645
 QY 586 TATGTTAAAGAGCTTTACACCTTTTACAGAGAAAATGAGGCTTAAGAGTTGTGTAAGGCCA 645
 Db 646 TATATTGAAGATCTTTACTCTTACTACAGAAAAGTTGAGAGTACTAGCTGTGTTTCACCA 705
 QY 646 GATTACATGTCAGGCAACAGAGACATAAACTCAAGATGAGAGCAATCTGTATTCAGTCTG 705
 Db 706 AACTATATGCGACAGCAATTTGACATTATGAAAGATGAGGGCTATACTGTTGACTGG 765
 QY 706 CTGATTGAGTTCACTACAAAGTTTGAACCTGATGATGAGAGCGCTCTTCTTATGGTAAAC 765
 Db 766 CTTATTGAGTGTGATGACAAATTCGACCTCATGATGAGAGATTTGTTTCTCACTGCTCAAT 825
 QY 766 ATAATAGATAGATTCTTGGAAAAGGAGTGTTCACAGAAAGCACTCAACTGTTGCGA 825
 Db 826 CTTATAGACAGATTTTGGAAAAGCAGTCTGTGTTTGAAGAAGCTTCAGTTGTTGGT 885
 QY 826 GTCACAGCTATGCTGCTGCTGTTGTAATATGAGAGGATATCTGTTCAGTTGTTGAGGAC 885
 Db 886 TTAGTGGCAATGCTTTTGGCATGCAAGTATGAGGAAGTTTCAGTGCCTGTGTTGGAGAT 945
 QY 886 CTTGTGCTGATATCTGACCGTGCCTACACAAAAGGGCAAAATTTTGAAGATGGAAGTTG 945
 Db 946 CTAATTTCTATATCAGACAGACATACACCCGGAAGAGTTCTGGAATGGAAGGTG 1005
 QY 946 ATTCTGAACAGCTGAGTTTCAACATGCTGTTCACACCTTATGCTTCTTATGAGAGG 1005
 Db 1006 ATGGTCAATGCAATGAAGTTTAAACATATCTGTGCGCAGACGCTATGTTTTCATGAGAAG 1065
 QY 1006 TTTCTGAAAGCTGACAGATGCAGATAAACAGCTTTGAGTGTAGGCTCATTTTTCATGCTGAG 1065
 Db 1066 TTCTTAAAGCGGCTCAAGCAGACAGAAAACCTTGAGCTGTAGCTTTCTTCTTATTGAG 1125
 QY 1066 CTTCTGCTGGTAGAATACCAATGCTGAATATCGGCTTGCATCTGGCTGCTGCTGCG 1125
 Db 1126 CTATCTCTTGTGAATATGCAATGTGTAAGTTTCTCTCTTCTTCAACTAGCTGCGCTGCT 1185
 QY 1126 GTTATATGCTGACAGTGTGCTATCAATCGTTGCCAGCACTGGACAAAAGGTCTGGGAGTCT 1185
 Db 1186 GTCTATACAGCTCAATGCACTATGATGTGTGTGTCAACAGTGTGAGTGAACATGTAATGG 1245
 QY 1186 CATAGCAGATACACTAGGACCAACTCTGAGTGTGCTGAGGATGATGCTAGATTTTCAC 1245

Db 1246 CACACCACTACTCTGAAGATCAACTCTTAGAATGCTCTAGTTTAATGGTTGACTTTCAC 1305
QY 1246 CAGAAAGCTGGAACAGTAAGTCACTGGCGTGCACAGGAAGTACATCACTACAGTTC 1305
Db 1306 AAGAAAGCTGGACAGGGAACCTTACAGGAGCAGATAGGAAGTATTCACATCAAAATTT 1365
QY 1306 GGTTCGGTGGCCAGAGATTTTCCTCGCGAGTTCCTGCTGGAG 1347
Db 1366 AGCTATCTGCGAATGTGAACCAAGATTTCTTCTGGAG 1407

RESULT 11

LES243455 1999 bp mRNA linear PLN 29-AUG-2000
LOCUS Lycopersicon esculentum mRNA for cyclin B2 (CycB2 gene).

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

ORIGIN

Query Match 22.3%; Score 364.6; DB 8; Length 1999;

Best Local Similarity 60.9%; Pred. No. 1.8e-77;

Matches 613; Conservative 0; Mismatches 389; Indels 5; Gaps 1;

QY 526 GATGATTCGTATGATATTCACAGTGCAGACTCGGGAACCCGCTGCTGCAACAGAA 585

Db 862 GAGGAGCTGTAATAGATATCGACGGTGATGATGCAAGAACCATCTTGCAGCTGTGAA 921

QY 586 TATGTTAAGAGCTTTACACCTTTTACAGAGAAATAGAGCTTAAGAGTTGTGTAAGGCA 645
Db 922 TATGTTGGAGATTTTGTGTTAACTACAGAACATAGAGGTTAATAGCTGTCTCTCA 981
QY 646 GATTACATGTTCCAGCAACAAGACATAAATCTCAAAGATGAGAGCAATTTCTGATGACTGG 705
Db 982 TACTATATGGCAACAAGAGCTGACATCAATGAGAGATGCGGTCTATCTTGTGTTGACTGG 1041
QY 706 CTGATTGAGGTTCACTACAGTTTCAATGATGATGAGAGCTCTTCTTATGTTAAAC 765
Db 1042 CTAATTGAGTGATCATCAAGTTTGAGCTCAGGGAAGAGAGCTTGTCTTGTGACCTCAAT 1101
QY 766 ATAATAGATAGATTTCTTGAAAGGAAGTGGTTCCAGGAAGAACTCAACTGTTGGA 825
Db 1102 TTGATTGACCGGTTCTTGAGAAACAAGGCTTTGTCAGAAAGAGCTCCAGCTTGTGGA 1161
QY 826 GTACAGCTATGCTGCTGCTTGTGTAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGAC 885
Db 1162 TTGGTTGCAATGCTACTAGCATGCAAGTATGAGGAGTTTGTCTTCCATGTTGAGGAT 1221
QY 886 CTGTGCTGATATCTGACCGTCTTACACAAAGGGCAAAATTTAGAAATGGAAGTTG 945
Db 1222 CTGTTGTTGATTTGGACAAAGCTTATACAGGAAGGAGTTTCTTGAATGGAAGCATG 1281
QY 946 ATTCGAACAGCTGCTGAGTTTCAACATGCTGTTCCAAACCTTATGCTTCTCATGAGAGG 1005
Db 1282 ATGCTCAACACATGCTGAGTTTAAATATGCTGTCCTCAACTGTCATGCTTTTATGCAAGA 1341
QY 1006 TTTCTGAAAGCTGACAGATGACAGATTAACAGCTTTGAGCTAGCTGCTTCTTCTGCTGGAG 1065
Db 1342 TATCTAAGGCTGCTCAATGTCAGAGGAGTTTGTCTGCTTCTTCTGTTGAG 1401
QY 1066 CTCTGCTTGGTGAATACCAATGCTGAATATGCGCTTCCATCTGCTGCTGCTGCTGCTG 1125
Db 1402 CTTTGGCTTGTGAGTATGAATGCTCAAAATTTCCACCATCTTCAATAGCTCTGCTGAGCA 1461
QY 1126 GTTTATACGTCACAGTGTGCTTCAATCGTTCAGACTGTCAGCAAAAGTCTGCGAGTCT 1185
Db 1462 ATCTATACAGCTCAGACCACTTACCGTGTCCAGCTGTCAGCAAGAGCTGCGAGGTT 1521
QY 1186 CATGAGATACACTAGGACCAACTCTGAGAGTGTCTGAGATGATGATGATGATGATGATG 1245
Db 1522 CACACAACTGCTCAGAGATCAACTCTGAGAGTGTCTGAGATCAATTTGCTGCTACCA 1581
QY 1246 CAGAAGCTGGAACCACTAGCTCACTGCGGTGTCAGGAGTACAGTACCTACAGTTC 1305
Db 1582 CAGAGGCGAGCAACAGGAACTACAGGGGTACATAGGAATACAGCATATCGAATTT 1641
QY 1306 GGTTCGCTGCGCAAGATTTTGGCTGCGAGTTTCTGCTGAGTTCGAGGAGGACACCGCT 1365
Db 1642 GGGTATGCGACCAAGTGTGAGCTGCGCTGCTTCTTGTGTCAGCAGACACAAGATAGAG 1701
QY 1366 CTTTCAGTGA-----AAGTGTGAATGAGCTTATCACTGCTGCTGCTGCTGCTGCTGCT 1420
Db 1702 AGAAGAGGGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1761
QY 1421 TTTTGAATATCTCCATGAACAGATGCAAGAAACATCTGTTGATGTTGCTGCTGCTGCTGCT 1480
Db 1762 GGTGATGGAATTTTATAGGAAGATACTTAGCAACTAAATGTTGCTGCTGCTGCTGCTGCT 1821
QY 1481 CATGGAATTTCTTGGAGAGTATGATTAACAACTTTTTTTTATCT 1527
Db 1822 CATTTATTTCTTTTATAGAGTTCATTTATTATTGTCACCTTTTACTATGT 1868

RESULT 12

AX449282

LOCUS

DEFINITION

AX449282

AX449282

AX449282

AX449282

AX449282

AX449282

AX449282

AX449282

AX449282

AX449282

AX449282

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE Inze, D., Boudolf, V., de Veylder, L., Acosta, J.A. and Magyar, Z.
AUTHORS Nucleic acid molecules encoding plant cell cycle proteins and uses
TITLES therefor
JOURNAL Patent: WO 0185946-A 1 15-NOV-2001;
CropDesign N.V. (BE)
FEATURES
source 1..1255
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
ORIGIN
Query Match 21.8%; Score 357; DB 6; Length 1255;
Best Local Similarity 63.7%; Pred. No. 1.2e-75;
Matches 543; Conservative 0; Mismatches 310; Indels 0; Gaps 0;
QY 496 GCGACAGAGCAAGACATATTGACGAGAGATGAAATTCCTCATGGATTTGACAGTGA 555
Db 172 GAGATTGAAATGGAAGATGACAGCAAGAGAGAGCCCTGTGATGATATTGATCCCTGT 231
QY 556 GACTCGGGGACCCGCTTGTGCAACAGAGATATGTTAAAGAGCTTTACACCTTTTACAGA 615
Db 232 GATAGAAATATCTTTGGCTGGCTGGTGAATATATCATGATGATGATGATGATGATGAT 291
-QY 616 GAAATGAGGCTAAGAGTTGTGTGAGGCCAGATTACATGTCAGGCCCAACAGACATAAC 675
Db 292 AATTTTGAAGAACTTAGTTGCGTGCCTCTTAATATGATGATGATGATGATGATGATGAT 351
QY 676 TCAAGATGAGCAATTCGATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
Db 352 GAGAGATGAGAGAAATCCCTCATGCTGTTGATGATGATGATGATGATGATGATGATGAT 411
QY 736 ATGGATGAGAGCTCTTTCTTATGTTAATGATGATGATGATGATGATGATGATGATGATGAT 795
Db 412 ATGGAGGAACTCTTTATCTCACATCAATGATGATGATGATGATGATGATGATGATGATGAT 471
QY 796 GTTCCAGGAGAGAGCTACAACTGTTGAGTGCAGCTATGCTGCTGCTGCTGCTGCTGCTGCT 855
Db 472 ATCGTGAGGAAAGCTTCAGCTGTGTTGGTGTACTGCTTGTGCTGCTGCTGCTGCTGCTGCT 531
QY 856 GAGGAGTATCTGTTCCAGTGTGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACA 915
Db 532 GAAGAGTTTCAGTTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 591
QY 916 AAAGGGCAATTTTAGAAATGGAAGTTGATCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
Db 592 AGAAGAGAGTGTGATATGAGAGAGCTAATGGCCCAACCTTGCAATTTCAATTTCTCT 651
QY 976 GTTCCACACCTTATGCTTCTCATGAGAGGTTTCTGAAAGCTGCAGATGAGATAAACAAG 1035
Db 652 CTACCAACTCCATATGTTTCAAGACGATTTCTCAAGCTGCCAATCTGACAGAGAG 711
QY 1036 CTTGAGTGTAGGCTCAATTTTCACTGCTGAGCTCTGCTGTTGTTAGATAACCAATGCTGAAT 1095
Db 712 CTTGAGATTTTATCATTTTATGATGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
QY 1096 TATCGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1155
Db 772 TATTTTCACTAAGCTGGGGCTCGAGCAATCTACACTGCTCAGTGTACACTTAAGGGA 831
QY 1156 TGCAGAGCTCGGACAAAGGTTGCGAGTCTCATAGAGATACACTAGCGACCACTGCTG 1215
Db 832 TTTGAAGAATGGAGCAAAACCTGTGAGTTTTCACAGAGCTACACGAAAGAGAGCTACTG 891
QY 1216 GAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1275
Db 892 GCATGTGCGAGAAAGATGTTGCTTTTCCATCAGAGCGAGGACAGGAGAGCTTCACAGGA 951

QY 1276 GTGCACAGAGTACAGTACCTTACAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1335
Db 952 GTTCACAGAGTACACACATCTAAGTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
QY 1336 TTCCTGCTGGAGT 1348
Db 1012 TTCCTGATTAAT 1024
RESULT 13
ZMU10076
LOCUS Zea mays B73 cyclin III2m mRNA, complete cds. PLN 27-JUL-1994
DEFINITION Zea mays B73 cyclin III2m mRNA, complete cds.
ACCESSION U10076
VERSION U10076.1 GI:516547
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1603)
AUTHORS Renaudin, J.P., Colasanti, J., Rime, H., Yuan, Z. and Sundaresan, V.
TITLES Cloning of four cyclins from maize indicates that higher plants
have three structurally distinct groups of mitotic cyclins
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (15), 7375-7379 (1994)
MEDLINE 94316698
PUBMED 8041798
REFERENCE 2 (bases 1 to 1603)
AUTHORS Sundaresan, V.
TITLES Direct Submission
JOURNAL Submitted (25-MAY-1994) Venkatesan Sundaresan, Cold Spring Harbor
Laboratory, P.O. Box 100, 1 Bungtown Road, Cold Spring Harbor, NY
11724, USA
FEATURES
source 1..1603
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="cycIII"
/tissue_type="ear"
/clone_lib="Lambda ZAPII, library of B. Veit and S. Hake"
/dev_stage="immature"
17..1291
/codon_start=1
/product="cyclin III2m"
/protein_id="AAA20236.1"
/db_xref="GI:516548"
/translation="MENLRQNCQHQGVMEGVKFAPEKANTNRRLSDIKNIIGGPHQ
HLAVSKALSEKPAASAAANAKDAQGVHRPVTRKFAATLATQPTVALLDPIGSERL
KRNADTAPHTPADMESTMTDDSPLMVSEMDMSPELKEIEMEDTEEAAPDIDSGD
AGNSLAVDYDEIYFRYRTEGASCVPTNYSQTDINEKMGILLIDWLEIHYKLE
LLEETLFTVNIIDRFLENVVRKKQLQAGVTAMLLACKYEVSVVVDLILICDR
AYTRADILEMERIVTNFNFSVPTFCFMRFLKAAQSEKKLELLSFMWIELSLVE
YEMIQFCPSMLAAAIYTAQCTINGFKSNKCCCELHTRYSEEHLMVCSRMWVLLHQRA
AHGKLITGVHRKYNTSRYSYAAKSEPPATFLDLA"
CDS
ORIGIN
Query Match 21.8%; Score 357; DB 8; Length 1603;
Best Local Similarity 64.9%; Pred. No. 1.2e-75;
Matches 528; Conservative 0; Mismatches 285; Indels 0; Gaps 0;
QY 541 GATATTGACAGTGCAGACTCGGGAAACCCGCTTGTGCAACAGAAATATGTTAAAGAGCTT 600
Db 479 GATATTGACAGTGTGATGACAGGAAATTTCTCTGCTGTGGCTGACTATGATGATGAAAT 538
QY 601 TACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAGGCCAGATATGATCTCCAGC 660
Db 539 TACAGATTTTACAGAAACTGAGGCTGCAAGCTCGCTCCCTCAAAATTTATGTCAAGC 598
QY 661 CAACAGACATAAACTCAAGATGAGAGCAATTTCTGATTGACTGGCTGATTGAGGTTTCA 720

```
Db 599 CAAACTGATATAAATGAGAGATCGGTGGCATTTCAATTGACTGGCTCATAGAGGTACAC 658
Qy 721 TACAAGTTTGAACATGATGAGATGACACGCTCTTTCTTATGTGTAACACATAATAGATAGATTC 780
Db 659 TACAAACTAGAGCTGTTGGAGGAGACCTTTTCTTACCCGTGAACATCATAGACAGATTC 718
Qy 781 TTGAAAGAGGAAGTGGTTCCAAAGGAAGATCAACTGGTTGAGTCAAGCTATGCTG 840
Db 719 TTGGCAGCTGAAAAATGTGGTGGGAAGAGCTTCAGTTAGCTGGTGAACCTGATGTTG 778
Qy 841 CTCCTGTTGAATATGAGGAGGTATCTGTTCCAGTCTGTTGAGGACCTTGTGCTGATATCT 900
Db 779 CTCGCTGCAAGTATGAGAAAGTGAAGCTACCTGTTGTCGAGATCTGATCTGTT 838
Qy 901 GACCGTGCCTACACAAAAGGCAAAATTTAGAAATGGAAGTGTGATTTCTGAACACGCTG 960
Db 839 GATCGTGATACACAAAGGCTGACATCTTGGAGATGGAGAGGAGATGATGAACACACTT 898
Qy 961 CAGTTCACATGCTGTTCCACACCTTATGCTTTCATGAAGAGGTTTCTGAAAGCTGCA 1020
Db 899 AATTTCATATGTGCGTGGCCGACTCCATACGTGTTTCATGAGAGGTTTCTTAAAGGAGCA 958
Qy 1021 GATCAGATAAACAGCTTGAGTACGCTCAATTTTTCATGCTGGAGCTCTGCTTGGTAGAA 1080
Db 959 CAATCAGAGAAAGAGCTCGAACTCCTGTCTTCTTCATGATCGAGTTGAGTCTGTGCAA 1018
Qy 1081 TACCAATGCTGAATATTCGSCCTTCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1019 TATGAGATGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1078
Qy 1141 TGTGCTATCAATCGTTGCGACATCGGCAAGAGTCTGCGAGTCTCATAGCAGATACACT 1200
Db 1079 TGCACCATATATGTTTCAAGTCTGGAACAAATGCTGTGAAGTGCACACAGATATTTCA 1138
Qy 1201 AGCAGACAACTCTGAGTGTCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1139 GAAGAACAATCTAATGGTTGCTCTAGGATGATGATGATGATGATGATGATGATGATGATG 1198
Qy 1261 AGTAAGCTCACTGGCGTGACAGAAAGTACAGTACCTACAAAGTTCGGTTCGGTGGCAAG 1320
Db 1199 GGGAACTTACAGGGTCCATAGAAAGTACAACTTCTAGATATAGTATGCTGCGAAA 1258
Qy 1321 ATTTTGCTGCGAGTTCCTGCTGGAGTGGGA 1353
Db 1259 TCGGAACCGCAACTTTCTTCTGATGCTGTA 1291
```

```
RESULT 14
AX449320 LOCUS AX449320 1715 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 39 from Patent WO0185946.
ACCESSION AX449320
VERSION AX449320.1 GI:21698067
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
AUTHORS Nucleic acid molecules encoding plant cell cycle proteins and uses
TITL therefor: WO 0185946-A 39 15-NOV-2001;
JOURNAL Patent: WO 0185946-A 39 15-NOV-2001;
FEATURES Location/Qualifiers
source 1..1715
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
ORIGIN
```

```
Query Match 21.8%; Score 357; DB 6; Length 1715;
Best Local Similarity 63.7%; Pred. No. 1.2e-75;
Matches 543; Conservative 0; Mismatches 310; Indels 0; Gaps 0;
Qy 496 GGGCAGAGAGAACAGGACATTATGAACGAAGATGAATTCCTCATGATATTGACAGTGA 555
Db 632 GAGATTGAAATGGAAGATGACAGACAAAGAGAGCCGTGATCGATATTGATGCCCTGT 691
Qy 556 GACTCGGGAAACCCCTTGTGCAACAGATATGTTAAAGAGCTTTACACCTTTTACAGA 615
Db 692 GATAAGAAATAATCCCTTTGGCTCGGCTTGAATATATCCATGATGATGATGATGATG 751
Qy 616 GAAATATGAGGCTATGAGTTGTGAGGCGCAGATACATGTCAGCCAAACAGACATAAAC 675
Db 752 AATTTTGAGAACTTAGTTTGGTGGCTCTTAACTATATGGAACATCAACAGATCTTAA 811
Qy 676 TCAAGATGAGAGCAATTTCTGATGACTGGCTGATGAGGTTTCACTACAGTTTGAATG 735
Db 812 GAGAGATGAGAGGAATCCTCATTCAGCTGGTTAATGAGGTGCACTACAGTTTGAATG 871
Qy 736 ATGGATGAGCGCTCTTTCTTATGTAACATAATAGATAGATTTCTTGAAAAGGAAGTG 795
Db 872 ATGGAGGAACCTTTTATCTCAATCAATGTCATCGACAGATTCCTTGGCGTTCATCAA 931
Qy 796 GTTCCAAGGAAGAGCTACAACTGGTTCGAGTCAAGCTATGCTGCTCGCTTGTAAATAT 855
Db 932 ATCGTGAGGAAAAGCTTCAGCTTGTGGTGTACTGCTTTGTGCTTGCATGTAAATAT 991
Qy 856 GAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTCCCTACACA 915
Db 992 GAAGAAGTTTCAGTTCCAGTGGTAGATGATCTCATCTTGTATCTTGAACAAGCTTACTCT 1051
Qy 916 AAGAGGCAAAATTTTGAAGATGGAAGTGTGATTTTGAACAGCTGCACTTCAACATGTCT 975
Db 1052 AGAAGAGAGTCTAGATATGAGAGAGCTAATGGCCAAACACCTTGCAATTCATTTCTCT 1111
Qy 976 GTTCCAACACCTTATGCTTCTCATGAGAGGTTTCTGAAGCTGCGAGATGCGAGATAACAG 1035
Db 1112 CTACCAACTCCATATGTTTTCATGAAGAGATTTCTCAAAGCTGCCCAATCTGCAAGAG 1171
Qy 1036 CTGAGCTAGCTCATATTTTTCATGCTGGAGTCTGCTTGGTAGAATACCAATGCTGAAT 1095
Db 1172 CTGAGATTTTATCTTCTTATGATCGAGCTTTCCTTGTGGAGTATGAGATGCTAGAG 1231
Qy 1096 TATCGGCTTCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1155
Db 1232 TATCTTCCATCTAAGCTGCGGCTCAGCAATCTACCTGCTCAGTGTACACTTAAAGGA 1291
Qy 1156 TGCCAGCACTGACAAAGGTCTGCGAGTCTCATAGCAGATACACTAGCGAACCACTCCTG 1215
Db 1292 TTTGAGATGAGCAAAACCTGTGAGTTTCACAGGCTACACGAAAACAGCTACTG 1351
Qy 1216 GAGTGTCTGAGGATGATGATGATTTTTCACAGAGGCTGGAAACAGTAAAGTCACTGGC 1275
Db 1352 GCATGTGCGAGAAAGATGTTTCTTCCATCAAGAGGAGGAAACAGGGAAGTCAAGGA 1411
Qy 1276 GTGCAAGAGAGTACAGTACCTACAGTTTCGCTGCGCAAGATTTTGCTGCGCAG 1335
Db 1412 GTTCACAGAAAGTACACACATCTAAGTTCTGCTGCTGCAAGACTGAACCAAGCTGG 1471
Qy 1336 TTCTGCTGCTGAGT 1348
Db 1472 TTCTGATTTAAT 1484
```

```
RESULT 15
AX449286 LOCUS AX449286 1287 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 5 from Patent WO0185946.
ACCESSION AX449286
VERSION AX449286.1 GI:21698033
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE
```

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
Inze, D., Boudolf, V., de Veylder, L., Acosta, J. A. and Magyar, Z.
Nucleic acid molecules encoding plant cell cycle proteins and uses
therefor
Patent: WO 0185946-A 5 15-NOV-2001;
CropDesign N.V. (BE)
FEATURES
Location/Qualifiers
source 1..1287
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
ORIGIN
Query Match 21.8%; Score 356; DB 6; Length 1287;
Best Local Similarity 63.9%; Pred. No. 2e-75;
Matches 539; Conservative 0; Mismatches 305; Indels 0; Gaps 0;
QY 501 AGAGAACAGGACATTATGAACAGAGATGAATTGCTCATGGATATTGACAGTGCAGACTC 560
Db 426 AGTTGAGATCGAGGATGAACAGTGGAGAACCGATCGTGGATATCGATGCTTTAGACTC 485
QY 561 GGGGAACCCGCTTGTGCAACAGATATGTTAAAGAGCTTTTACACTTTTACAGAGAAAA 620
Db 486 GAAGAACTCGCTTGGCGCTGTTGAATATGTTCAAGATCTTTACGCACTTTTACAGAACAT 545
QY 621 TGAGGCTAAGAGTTGTGAAGCCAGATTACATGTCCAGCCCAACAGACATTAACCTCAA 680
Db 546 GGAGAGATTAGTTGTGTTCCAGTACATATATGATGCAACAAATCGACTTAAACGAGAA 605
QY 681 GATGAGAGCAATCTGATGACTGGCTGATTGAGGTTCACTCAAGTTTGAACATGATGA 740
Db 606 GATGAGAGCAATCTAATCGACTGGTTAATCGAGGTACATGACAGTTTGTCTGATGA 665
QY 741 TGAGAGCTCTTTCTTATGTTAAACATAATAGATAGATTCTTGGAAAAAGAGTGTCTCC 800
Db 666 CGAGACACTGTTCTGACAGTGAATCTGATAGATAGATTCTTGTCCAAAGCAAAATGTTAT 725
QY 801 AAGGAGAGACTCAACTGTTGGAGTCAAGCTATGCTGCTGCTTGTAAATATGAGGA 860
Db 726 GAGAAAGAGCTTCAGCTGTAGGGTTAGTACGTTTGTGTTAGCTTTGTAAGTATGAGGA 785
QY 861 GGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACAAAGG 920
Db 786 GGTTCGGTTCCTGTTGTCGAGATTAGTACTCAATTCGACAAAGCGTATACGAGGAA 845
QY 921 GCRAATTTAGAAATGAAAAGTTGATCTGACACGCTGCTCAAGCATGCTGTTCC 980
Db 846 CGATGTTCTAGAGATGAGAAAAACAATGTTGAGTACTTTTGCATTTCAATATCTCGTTACC 905
QY 981 AACACCTTATGCTTTCATGAAGAGGTTTCTGAAAGCTGCAGATGCAGATAAACAGCTTGA 1040
Db 906 GACACAATACCCGTTCTTGAAGATTCTCTCAAGGAGCTCAAGCAGACAAAGAGTGA 965
QY 1041 GCTAGCGTCAATTTTCAATGCTGAGGCTCTGCTGGTAGAATACCAATGCTGATATCG 1100
Db 966 GGTCTTGGCGTCTGTTTGTATCGAGCTTGCCCTTGTGGAGTACGAGATGCTTCGGTTTC 1025
QY 1101 GCCTTCGCATCTGCTGCTGCGGTTTATCTGACAGTGTGCTATCAATGCTTGCCA 1160
Db 1026 ACCATCACTAGCTGCCACATCTGTGACACTGCTCAATGTACACTTGTATGTTCCAG 1085
QY 1161 GCACGTGACAAAGTCTGCGAGTCTCATAGCAGATACACTAGGACCAACTCTGGAGTG 1220
Db 1086 GAAATGGAACAGTACATGTGAATCCATTTGTCATTACTCTGAAGACCAAGCTCAATGAATG 1145
QY 1221 CTCGAGGATGATGTTAGATTTTCCAGAGGCTGGAAACAGTAAGCTCACTGGCGTGA 1280
Db 1146 TTCACGGAAGCTGTGAGTCTGCATCAGAGGCGGCGACAGGAACCTTACAGAGATATN 1205

QY 1281 CAGGAGTACAGTACTCAAGTTCGGTTGCGTGGCCAGATTTTGGCTTGGCAGTTCCT 1340
Db 1206 TAGGAAGTACAGCACAGCRAAATTTGGTTACATAGCAMAATGGAAGCTGCACACTTCT 1265
QY 1341 GCTG 1344
Db 1266 AGTG 1269

Search completed: March 20, 2004, 21:50:17
Job time : 6491 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 15:08:29 ; Search time 674 Seconds
(without alignments)
10311.650 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1636
Sequence: 1 tcacggggtctctccgtccg.....aaaaaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1275	77.9	1275	3 AAC83108	AAC83108 DNA encod
2	357	21.8	1255	6 AAS96272	AAS96272 Arabidops
3	357	21.8	1715	6 AAS96310	AAS96310 Arabidops
4	356	21.8	1287	6 AAS96276	AAS96276 Arabidops
5	301.2	18.4	627	9 ADD15948	ADD15948 CDNA (Seq
6	223.4	13.7	274	7 ABX81803	ABX81803 Corn ear-
7	214.6	13.1	1338	6 ABZ12384	ABZ12384 Arabidops
8	197	12.0	1980	3 AAC83106	AAC83106 DNA encod
9	191.8	11.7	1385	3 AAC42253	AAC42253 Arabidops
10	161.4	9.9	1553	3 AAC77911	AAC77911 Human can
11	160.2	9.8	1507	4 AAH14263	AAH14263 Human cDN
12	160.2	9.8	1532	8 ACH03960	ACH03960 Human cDN
13	160.2	9.8	1981	2 AAV83711	AAV83711 Nucleic a
14	158.6	9.7	1401	3 ABK12023	ABK12023 Human cyc
15	155.6	9.5	2308	6 AB199379	AB199379 Mouse isc
16	155.4	9.5	1452	2 AAQ37741	AAQ37741 Complete
17	155.4	9.5	1452	2 AAV30100	AAV30100 Complete
18	155.4	9.5	1452	6 AAV162877	AAV162877 Breast ca
19	155.4	9.5	1452	6 AB167953	AB167953 Ovary can
20	155.4	9.5	1452	6 AB165385	AB165385 Lung can
21	155.4	9.5	1452	6 AB162871	AB162871 Colon ade
22	155.4	9.5	1452	6 AB165823	AB165823 Lung can
23	155.4	9.5	1452	6 ABT10909	ABT10909 Human bre

24	155.4	9.5	1452	6 ABN95810	ABN95810 Gene #230
25	155.4	9.5	1568	4 AAI59816	AAI59816 Human pol
26	155.4	9.5	1570	4 AAI58030	AAI58030 Human pol
27	155.4	9.5	1578	7 ACC51016	ACC51016 Human bla
28	155.4	9.5	7477	7 ACC44992	ACC44992 Vector pc
29	155.4	9.5	7477	8 ADB85371	ADB85371 Vector DN
30	153.8	9.4	1302	2 AAT41775	AAT41775 Human cyc
31	152	9.3	1278	7 ABT18843	ABT18843 Aspergill
32	152	9.3	1347	7 ABT18249	ABT18249 Aspergill
33	152	9.3	1464	7 ABT20663	ABT20663 Aspergill
34	152	9.3	1577	7 ABT20065	ABT20065 Aspergill
35	152	9.3	3347	7 ABT17655	ABT17655 Aspergill
36	152	9.3	3577	7 ABT19469	ABT19469 Aspergill
37	139.2	8.5	659	7 ABZ19165	ABZ19165 Group III
38	128.4	7.8	625	9 ADD17214	ADD17214 DNA (Seq)
39	125.6	7.7	1646	2 AAQ13385	AAQ13385 Human cyc
40	125.6	7.7	1649	2 AAV16888	AAV16888 Human pro
41	125.6	7.7	1649	2 AAX26023	AAX26023 Prostate
42	125.6	7.7	1649	3 AAZ87508	AAZ87508 Cyclin A
43	125.6	7.7	1649	4 AAS03727	AAS03727 Biomarker
44	125.6	7.7	1649	6 ABL69120	ABL69120 Kidney ca
45	125.6	7.7	2207	4 ABL20111	ABL20111 Drosophila

ALIGNMENTS

RESULT 1

AAC83108
ID AAC83108 standard; DNA; 1275 BP.

XX AAC83108;

XX 23-FEB-2001 (first entry)

XX DNA encoding a protein involved in the cell cycle SEQ ID 29.

XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
KW cotton; rice; barley; millet; ds.

XX Zea mays.

XX WO200065040-A2.

XX 02-NOV-2000.

XX 13-APR-2000; 2000WO-US009975.

XX 22-APR-1999; 99US-0130849P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Helentjaris TG, Habben JE, Sun Y;

XX WPI; 2000-687333/67.

XX P-PSDB; AAB35801.

XX Nucleic acids useful for producing transgenic plants, preferably maize,
PT with increased cell cycle gene activity, preferably activity of cyclin
PT and/or cyclin-dependent kinase.

XX Claim 1; Page 104-106; 122pp; English.

XX Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
AAC835806 which are involved in regulating the cell cycle. The protein and
DNA sequences have been isolated from Zea mays (corn), and the invention
also includes oligonucleotides AAC83114 - AAC83139 which are related to
the cell cycle polynucleotides. The cell cycle polynucleotide sequences
are useful for producing transgenic plants such as maize, soybean,
sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
millet with increased levels of cell cycle gene activity, such as
activity of cyclin and cyclin-dependent kinases. The DNA sequences are

CC also useful as probes for detecting deficiencies in the level of mRNA in
 CC screening for desired transgenic plants, for detecting mutations in the
 CC gene, for monitoring upregulation of expression or changes in enzyme
 CC activity in screening assays of compounds, for detecting any number of
 CC allelic variants, orthologs or paralogs of the gene, and site-directed
 CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
 CC recombinant expression of the encoded polypeptides and as immunogens for
 CC preparing and screening antibodies. A transgenic plant comprising an
 CC expression cassette including a cell cycle regulatory gene is useful for
 CC assaying enzyme agonists and antagonists, and as immunogens or antigens
 CC to obtain antibodies. The antibodies are useful in assaying and isolating
 CC levels of cell cycle regulatory proteins, for identifying and isolating
 CC nucleic acids from expression libraries, for identifying homologues of
 CC polypeptides from other species, and for purification of the proteins
 XX
 SQ Sequence 1275 BP; 350 A; 291 C; 353 G; 281 T; 0 U; 0 Other;
 Query Match 77.9%; Score 1275; DB 3; Length 1275;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 109 ATGGCGCGCGCGCGCTGACAGAAACAGAGACCGCGCGGAGGAGCCGCCAGGC 168
 Db 1 ATGGCGCGCGCGCGCTGACAGAAACAGAGACCGCGCGGAGGAGCCGCCAGGC 60
 QY 169 GTCCGAGACATGCGCGCGCGCGCTGACAGAAACAGAGACCGCTCGTGGGCGTCC 228
 Db 61 GTCCGAGACATGCGCGCGCGCGCTGACAGAAACAGAGACCGCTCGTGGGCGTCC 120
 QY 229 CCGTACCCCTACCGCGTCCGCGCGCGCGCTGACAGAAACAGAGACCGCGCGGAGG 288
 Db 121 CCGTACCCCTACCGCGTCCGCGCGCGCGCTGACAGAAACAGAGACCGCGCGGAGG 180
 QY 289 CAGCCAGCGTGTGACAGAGCGCGCGCGCTGACAGAAACAGAGACCGCTCGTGGGCG 348
 Db 181 CAGCCAGCGTGTGACAGAGCGCGCGCGCTGACAGAAACAGAGACCGCTCGTGGGCG 240
 QY 349 AAGGGCCAACTGAATGTGAGCGATGCGTGTGATGATGATGATGATGATGATGATGAT 408
 Db 241 AAGGGCCAACTGAATGTGAGCGATGCGTGTGATGATGATGATGATGATGATGATGAT 300
 QY 409 AAGGAATCAGTAGCGGATGCGCGCGCGCTGATGATGATGATGATGATGATGATGATGAT 468
 Db 301 AAGGAATCAGTAGCGGATGCGCGCGCGCTGATGATGATGATGATGATGATGATGATGAT 360
 QY 469 GGTAGTGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
 Db 361 GGTAGTGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 529 GAATGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
 Db 421 GAATGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAGGCGCAGAT 648
 Db 481 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAGGCGCAGAT 540
 QY 649 TACATGTCACGCAACAGACATTAAGTCAAGATGAGGCAATCTGATGATGATGATGATGAT 708
 Db 541 TACATGTCACGCAACAGACATTAAGTCAAGATGAGGCAATCTGATGATGATGATGATGAT 600
 QY 709 ATTGAGGTTCACACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 768
 Db 601 ATTGAGGTTCACACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 769 ATAGATGATTTCTGGAAAGAGAGTGTTCAGAGGAGAGCTACAGCTGTTTGGAGTC 828
 Db 661 ATAGATGATTTCTGGAAAGAGAGTGTTCAGAGGAGAGCTACAGCTGTTTGGAGTC 720
 QY 829 ACAGTATGCTGCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 888
 Db 721 ACAGTATGCTGCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGCAAAATTTAGAAATGAAAAGTTGATT 948
 Db 781 GTGCTGATATCTGACCGTGCCTACACAAAGGGCAAAATTTAGAAATGAAAAGTTGATT 840
 QY 949 CTGAACACGCTGACGTTCAACATGCTGTTCCACACCTTATGCTTTCATGAGAGGTTT 1008
 Db 841 CTGAACACGCTGACGTTCAACATGCTGTTCCACACCTTATGCTTTCATGAGAGGTTT 900
 QY 1009 CTGAAGCTGACAGATGACAGATGACAGATGACAGATGACAGATGACAGATGACAGAT 1068
 Db 901 CTGAAGCTGACAGATGACAGATGACAGATGACAGATGACAGATGACAGATGACAGAT 960
 QY 1069 TGCCTGTTAGAAATACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1128
 Db 961 TGCCTGTTAGAAATACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 QY 1129 TATACCTGACAGTGTGCTATCAATCGTTGCCACGACTGACAAAGAGTCTGCGAGTCTCAT 1188
 Db 1021 TATACCTGACAGTGTGCTATCAATCGTTGCCACGACTGACAAAGAGTCTGCGAGTCTCAT 1080
 QY 1189 AGCAGATACACTAGGACCAACTCTCTGGAGTGTCTGAGGATGATGATGATGATGATGAT 1248
 Db 1081 AGCAGATACACTAGGACCAACTCTCTGGAGTGTCTGAGGATGATGATGATGATGATGAT 1140
 QY 1249 AAGCTTGGAAACAGTAAAGCTCACTGCGTGCACAGAGTACAGTACCTTACAGTTCCGT 1308
 Db 1141 AAGCTTGGAAACAGTAAAGCTCACTGCGTGCACAGAGTACAGTACCTTACAGTTCCGT 1200
 QY 1309 TGGCTGCGCCAAAGATTTTGGCTGCGCAGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1368
 Db 1201 TGGCTGCGCCAAAGATTTTGGCTGCGCAGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 QY 1369 TCAGGTGCAAACTAG 1383
 Db 1261 TCAGGTGCAAACTAG 1275
 RESULT 2
 AAS96272 standard; cDNA; 1255 BP.
 ID AAS96272 standard; cDNA; 1255 BP.
 AC AAS96272;
 XX 26-FEB-2002 (first entry)
 DT Arabidopsis cDNA encoding partial cell cycle protein CCP1.
 DE Cell cycle protein; CCP, ss; cell cycle regulation; herbicide;
 KW plant growth regulator; plant development; abiotic stress; biotic stress;
 KW nutrient deprivation; pathogen attack; crop yield.
 XX Arabidopsis thaliana.
 OS WO200185946-A2.
 PN 15-NOV-2001.
 PD 14-MAY-2001; 2001WO-IB001307.
 PF 12-MAY-2000; 2000US-0204045P.
 PR (CROP-) CROPDESIGN NV.
 PA Inze D, Boudolf V, De Veylder L, Acosta JAT, Magyar Z;
 PI WPI; 2002-062249/08.
 DR P-PSDB; AAU72482.
 XX New cell cycle protein and nucleic acid molecule encoding it useful for
 PT regulating cell cycle progression in plants and for identifying
 PT modulators which are useful as herbicides or plant growth regulators.
 XX Claim 38; Fig 1; 316pp; English.

XX CC The invention relates to a novel cell cycle protein (CCP) and the
CC polynucleotides encoding them. CCP is useful for identifying a compound
CC which modulates the activity of the polypeptide and which binds to the
CC polypeptide and an anti-CCP antibody is useful for detecting the presence
CC of CCP in a sample. A CCP modulator is useful for modulating the cell
CC cycle or growth of a plant such as *Arabidopsis thaliana*, rice, wheat,
CC maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP
CC nucleic acid and polypeptide molecules are useful as modulating agents in
CC regulating cell cycle progression in plants. CCP is useful to treat
CC disorders characterised by insufficient or excessive production of CCP
CC protein or production of CCP protein forms which have decreased or
CC aberrant activity. Compounds that bind to or modulate the activity of CCP
CC polypeptide are useful as herbicides or plant growth regulators. The
CC polynucleotide is useful for modifying cell fate, plant development,
CC plant morphology, biochemistry and/or physiology, the length of the G1,
CC S, G2 and/or M phase of the cell cycle of a plant, initiation, promotion,
CC stimulation or enhancement of cell division, DNA replication, seed set,
CC seed size, seed development, tuber, fruit, leaf formation, shoot and root
CC initiation and/or development, nodule function, dwarfism in plants,
CC senescence, tolerance or resistance to stress. CCP, the polynucleotide
CC and the anti-CCP antibody are useful in agriculture to modulate the
CC protein levels or activity of a protein involved in the cell cycle due to
CC environmental conditions, including abiotic stress such as cold, nutrient
CC deprivation, heat, drought, salt stress, or biotic stress such as
CC pathogen attack, to modulate e.g. enhance crop yields, and attenuate
CC plant architecture, plant quality traits, plant reproduction and seed
CC development, endoreduplication in storage cells, storage tissues and/or
CC storage organs of plants or its parts. CCP is useful as an immunogen to
CC generate antibodies. CCP protein is useful to screen for naturally
CC occurring CCP substrates. The polynucleotide is useful for expressing CCP
CC protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to
CC modulate CCP activity. The present sequence encodes a CCP protein of the
CC invention

QY	976	GTTCACACACTTATGTTCTTCATGAAGAGGTTTCTGAAGCTGCAGATGCAGATAAACAG	1033
Db	652	CTACCAACTCCATATGTTTTCATGAACGATTTCTCAAAGCTGCCAATCTGCAAGAAG	711
QY	1036	CTTGAGCTACGCTCATTTTTCATGCTGGAGCTCTGTTGTGTAGAAATACCAAAATGCTGAAT	1095
Db	712	CTTGAGATTTTATCAATCTTTATGATCGAGCTTTGCCTTGTGGAGTATGAGATGCTAGAG	771
QY	1096	TATCGGCTTCGCATCTGGCTGCTGCTGCGGTTTATCTGCACAGTGTGCTATCAATCGT	1155
Db	772	TATCTTCCATCTAAGCTGGCGGCTCAGCAATCTACATGCTCAGTGTACACTTTAAGGA	831
QY	1156	TGCAGCACTGGACAAAGGCTCTCGAGTCTCATAGCAGATACACTAGCGACCACTCGT	1215
Db	832	TTTGAAGAATGGAGCAAAACCTGTGATTTTCCACAGGCTTACCAAGAAAACAGCTACTG	891
QY	1216	GAGTGCTCGAGGATGATGGTAGATTTTTCACCAAGAGGCTGGAACCACTAAGCTCAGTGGC	1275
Db	892	GCATGTGCGAGAAAGATGGTTGCTTTCCATCACAGGACAGGAAAGCTCACAGGA	951
QY	1276	GTGCACAGGAAGTACAGTACTACAGATTCGGTTGCTGCGCAAGATTTTGCCTGCGCAG	1335
Db	952	GTTTCACAGAAGTACACACATCTAAGTTCTGTCTCATGCTCAAGAACTGAACCAAGCTGGG	1011
QY	1336	TTCTGCTGGAGT	1348
Db	1012	TTTCTGATTTAAT	1024
RESULT 3			
AAS96310			
XX	AAS96310 standard; cDNA; 1715 BP.		
XX	AAS96310;		
XX	26-FEB-2002 (first entry)		
XX	Arabidopsis cDNA encoding cell cycle protein CCP1.		
XX	Cell cycle protein; CCP; ss; cell cycle regulation; herbicide;		
XX	plant growth regulator; plant development; abiotic stress; biotic stress;		
XX	nutrient deprivation; pathogen attack; crop yield.		
XX	Arabidopsis thaliana.		
XX	WO200185946-A2.		
XX	15-NOV-2001.		
XX	14-MAY-2001; 2001WO-IB001307.		
XX	12-MAY-2000; 2000US-0204045P.		
XX	(CROP-) CROPDESIGN NV.		
XX	Inze D, Boudolf V, De Veylder L, Acosta JAT, Magyar Z;		
XX	WPI; 2002-062249/08.		
XX	P-PSDB; AAU72520.		
XX	New cell cycle protein and nucleic acid molecule encoding it useful for		
XX	regulating cell cycle progression in plants and for identifying		
XX	modulators which are useful as herbicides or plant growth regulators.		
XX	Claim 38; Fig 1; 316pp; English.		
XX	The invention relates to a novel cell cycle protein (CCP) and the		
XX	polynucleotides encoding them. CCP is useful for identifying a compound		
XX	which modulates the activity of the polypeptide and which binds to the		
XX	polypeptide and an anti-CCP antibody is useful for detecting the presence		
XX	of CCP in a sample. A CCP modulator is useful for modulating the cell		
XX	cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, CC		
XX	maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP		

nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein or production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polypeptide are useful as herbicides or plant growth regulators. The polynucleotide is useful for modifying cell fate, plant development, plant morphology, biochemistry and/or physiology, the length of the G₁, S, G₂ and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, seed size, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, nodule function, dwarfism in plants, senescence, tolerance or resistance to stress. CCP, the polynucleotide and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to environmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally occurring CCP substrates. The polynucleotide is useful for expressing CCP protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence encodes a CCP protein of the invention.

Query Match 21.8%; Score 357; DB 6; Length 1715; Best Local Similarity 63.7%; Pred. No. 5.7e-84; Matches 543; Conservative 0; Mismatches 310; Indels 0; Gaps 0;

496 GCGACAGACAGACAGACATTATGACGAGAGATGCTCATGATATTGACAGTGA 555
Db |||||
632 GAGATTGAATGAATGACAGACAGACAGAGAGCCCTGTGATGATATTGATCCCTGT 591
Qy * 556 GACTCGGGGACCCGCTTCTGTCACACAGAAATATGTTAAAGAGCTTTACACCTTTACAGA 615
Db |||||
692 GATAAGAAATATCCTTTGGCTGGCTGGAATATATATCCATGATATGATACCTTTACAA 751
Qy * 616 GAAATGAGGCTTAAGATTGTTGTAAGCCAGATTACATGCCAGCCAAACAGACATAAC 675
Db |||||
752 AATTTTGAGAACTTATAGTTCGGCTCTTAATATATGATGACAAATCAACAGATCTTAAT 811
Qy * 676 TCAAAGATGAGCAATTTCTGATTGCTGCTGATTGAGGTTCACTACAAAGTTTGAACGTG 735
Db |||||
812 GAGAGATGAGAGAAATCCTCAATTGCTGTTAAATGAGGTGCACCTACAAAGTTGAACGT 871
Qy * 736 ATGGATGAGAGCTCTTTCTTATGTTAAACATATAGATAGATTCTTGAAAGGAGGTG 795
Db |||||
872 ATGGAGGAACTCTTTATCTTCACAATCAATGTCATGACAGATTCTTGGGTTTCAATCAA 931
Qy * 796 GTTCCAGGAGAGAGCTTACAACTGGTTGGAGTCACAGCTATGCTGCTGCTGTTAAATAT 855
Db |||||
932 ATGCTGAGGAAAAGCTTCAGCTTGTGGTGTACTGCTTGTGCTTCATGATTAATAT 991
Qy * 856 GAGAGGATATCTGTTTCAGTTGTTGAGACCTTGTGCTGATATCTACCGTGCCTACACA 915
Db |||||
992 GAAGAGCTTTCAGTTCCAGTGGTAGATGATCTCATCTTGTATCTCTACAAAGCTTACTCT 1051
Qy * 916 AAAGGGCAATTTTGAAGAAATGGAAGCTTGAATCTGAACACGCTGCGAGTTCAACATGCT 975
Db |||||
1052 AGAGAGAGTGTAGATATGAGAGAGCTAATGCCACACCTTGGCAATTCATTTCTCT 1111
Qy * 976 GTTCCACACATTATGCTTCATGAGAGAGGTTTCTGAACTGAGATGACAGTAACAG 1035
Db |||||
1112 CTACCACTCCATATGTTTTCATGAACAGATTTCTCAAGCTCCCAATCTGCAAGAG 1171
Qy * 1036 CTTGAGCTAGGCTCATTTTTCATGCTGAGCTCTGCTTGTGTAAGAACCAATGCTGAAT 1095
Db |||||
1172 CTTGAGATTTAATCATTTCTTATGATGACGCTTGGCTTGGATGATGAGATGCTAGAG 1231

QY 1096 TATCGGCTTCGATCTGGCTGCTGGGTTTATCTGACACAGTGTGCTATCAATCGT 1155
Db |||||
1232 TATCTTCCATCTAAGCTGGGCGCTTCAGAAATCTACATGCTCACTTACACTTAAGGA 1291
QY 1156 TGCACGACTGACAAAGGCTCTGCGAGTCTCTATAGCAGATACACTAGGACCACTCCCTG 1215
Db |||||
1292 TTTGAGAAATGAGCAAAACCTGTGAGTTTACACAGGCTACACGAAACAGACTACTG 1351
QY 1216 GAGTCTCCAGATGATGATGATGATTTTACACAGAGGCTGGAAACAGTAAGTCTCACTGC 1275
Db |||||
1352 GCATGTCGAGAAAGATGTTCTTTCATCATCAGGAGGAAACAGGAGAGTTCACAGA 1411
QY 1276 GTCCACAGCAAGTACAGTACCTACAGTTTCGTTGCTGGCCAAAGATTTTGCTGCGGAG 1335
Db |||||
1412 GTTCACAGAAAGTACACACATCTAAGTTCTGCTGTCAGAAACTGACACAGCTGGG 1471
QY 1336 TTCTCTGCTGAGT 1348
Db |||||
1472 TTTCTGATTTAAT 1484

RESULT 4
AAS96276
ID AAS96276 standard; cDNA; 1287 BP.
XX
AC AAS96276;
XX
DT 26-FEB-2002 (first entry)
XX
DE Arabidopsis cDNA encoding cell cycle protein CCP5.
XX
KW Cell cycle protein; CCP; ss; cell cycle regulation; herbicide;
KW plant growth regulator; plant development; abiotic stress; biotic stress;
KW nutrient deprivation; pathogen attack; crop yield.
XX
OS Arabidopsis thaliana.
XX
PN WO200185946-A2.
XX
PD 15-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-IB001307.
XX
PR 12-MAY-2000; 2000US-0204045P.
XX
PA (CROP-) CROPPDESIGN NV.
XX
PI Inze D, Boudolf V, De Veylder L, Acosta JAT, Magyar Z;
XX
DR WPI; 2002-062249/08.
XX
DR P-PSDB; AAU72486.
XX
PT New cell cycle protein and nucleic acid molecule encoding it useful for
PT regulating cell cycle progression in plants and for identifying
PT modulators which are useful as herbicides or plant growth regulators.
XX
PS Claim 38; Fig 6; 316pp; English.
XX
CC The invention relates to a novel cell cycle protein (CCP) and the
CC polynucleotides encoding them. CCP is useful for identifying a compound
CC which modulates the activity of the polypeptide and which binds to the
CC polypeptide and an anti-CCP antibody is useful for detecting the presence
CC of CCP in a sample. A CCP modulator is useful for modulating the cell
CC cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat,
CC maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP
CC nucleic acid and polypeptide molecules are useful as modulating agents in
CC disorders characterised by insufficient or excessive production of CCP
CC protein or production of CCP protein forms which have decreased or
CC aberrant activity. Compounds that bind to or modulate the activity of CCP
CC polypeptide are useful as herbicides or plant growth regulators. The
CC polynucleotide is useful for modifying cell fate, plant development,
CC plant morphology, biochemistry and/or physiology, the length of the G₁,
CC

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 789.
DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
KW Arabidopsis thaliana.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX WO200216555-A2.
PN 28-FEB-2002.
XX 24-AUG-2001; 2001WO-US026685.
XX 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0254647P.
ER 22-JUN-2001; 2001US-0300111P.
XX (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Kreps J, Wang X, Zhu T;
PI WPI; 2002-304127/34.
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX Claim 144; SEQ ID NO 789; 577bp + Sequence Listing; English.
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX Sequence 1338 BP; 381 A; 281 C; 329 G; 347 T; 0 U; 0 Other;
SQ Query March 13.1%; Score 214.6; DB 6; Length 1338;
Best Local Similarity 54.5%; Pred. No. 3.1e-46;
Matches 452; Conservative 0; Mismatches 374; Indels 3; Gaps 1;
QY 516 TATGAACGAAGATGAATTCCTCATGGATATTGACAGTCAGCTCGGCGAACCCGCTTGC 575
DB 474 TATAGTCAACAAACCAAGATTATCGATATTGATGATCTGACAAAGATAACCATTTGGC 533
QY 576 TGCACAGATATGTTAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAGAGTTG 635
DB 534 TGCCTGGAGTATGTTGATGATATGATCTCTCTATTAAGAGTTGAGAGGAGTCA 593
QY 636 TGTAAAGCCAGATTACATGTCAGCCACCAAGACATAAATCAAGATGAGAGCAATTC 695
DB 594 GCCTAAGATG---TACATGCACATTCAGCTGAATGATGAGAGATGAGGCACTT 650
QY 696 GATTGACTGGCTGATGAGGTTCTACTACAAGTTTGAACCTGATGATGAGAGCTCTTTCT 755
DB 651 GATTGATGGTTACTAGAAGTTTCATCAAGTTTGAAGCTCAACCTTGAAGCTCTGTACCT 710
QY 756 TATGTTAAACATAATAGATAGATCTCTTGGAAAGAGAGTGTTCACAGGAGAGCTACA 815
DB 711 CACCGTCAACATCATTTGATGATCTCTCTCTGTGAAGCTGTCTTAAAGAGAGTTACA 770
QY 816 ACTGTTGAGTCAAGATATGCTGCTCTGCTTGTAAATATGAGGAGGTATCTGTTCCAGT 875
DB 771 GCTAGTGGGAATCAGTGCTGCTTGTATGCTTCCAAATATGAAGAAATCTGCCACCTCA 830
QY 876 TGTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACAAAGGCCAAATTTTAGAAT 935

DB 831 GGTAAACGATCTGGTGTATGTACCGCAATGCTTACAGTAGCAGACAGATTCGGTAT 890
QY 936 GGAAAAGTTGATTTGAAACACGCTGCAATCAATGCTCTGTTTCCAAACACCTTATGCTTT 995
DB 891 GGAGAAGGCAATTTCTTGGAAACCTCGAATGGTATTTTGACAGTCCGACTCAATACGCTTT 950
QY 996 CANTGAAGAGGTTTCTGAAAGCTGCGAGATGCGAGATAAACAGCTTGAGCTAGCGTCAATTTT 1055
DB 951 CTTTTCGCTTCATCAAAAGCTTCGATGCTGTGATCCAGAAATGAGATATGGTTCATT 1010
QY 1056 CATGCTGAGCTCTGCTTTGGTAGAATACCAATGCTGAATTAATCGGCTTCGCATCTGGC 1115
DB 1011 CTTTCTGAAATTTGGGATGATGATACGACACCTTGACGTTCTGCTCCCTCCATGCTTGC 1070
QY 1116 TGCTGCTGGGTTTATACTGACAGTGTGCTATCAATGTTGCCAGCAGCTGCAAAAGGT 1175
DB 1071 TGTCTCAGCTGTTTACCGGCAAGATGCTATTGAACAGTCCCTGCTGCTGAGCTGATAC 1130
QY 1176 CTGCGAGTCTCATAGCAGATACACTAGCGCAACTCTCTGAGTGTCTCGAGGATGATGTT 1235
DB 1131 ATTGCAGTTCCACACCGCTACACAGAGTCTGAGATTATGAGCTCTCTCTCTTTCG 1190
QY 1236 AGATTTTCCACAGAGGCTGGNACAGTAAGCTCACTGGCTGCGACAGGAGTACAGTAC 1295
DB 1191 TTTTCTTCACTCGAGATCGGTTGAGAGCAGGCTAGCTGAGTGTACAAAGAGTACTCGAA 1250
QY 1296 CTACAAGTTCCGTTGCGTGGCCAGATTTTGCCTGCGCAGTTCCTCTG 1344
DB 1251 GSCAGAGATGAGGTTGTTGTTATGTTTCTCGGCCAAGTCTCTCTT 1299
RESULT 8
AAC83106
ID AAC83106 standard; DNA; 1980 BP.
XX AAC83106;
AC AAC83106;
XX 23-FEB-2001 (first entry)
XX DNA encoding a protein involved in the cell cycle SEQ ID 21.
XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
KW cotton; rice; barley; millet; ds.
XX Zea mays.
XX WO200065040-A2.
XX 02-NOV-2000.
XX 13-APR-2000; 2000WO-US009975.
XX 22-APR-1999; 99US-0130849P.
XX (PION-) PIONEER HI-BRED INT INC.
XX Helentjaris TG, Habben JE, Sun Y;
XX WPI; 2000-587333/67.
XX P-PSDB; AAB35799.
XX Nucleic acids useful for producing transgenic plants, preferably maize,
PT with increased cell cycle gene activity, preferably activity of cyclin
PT and/or cyclin-dependent kinase.
XX Claim 1; Page 97-99; 122pp; English.
XX Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
CC AAB35806 which are involved in regulating the cell cycle. The protein and
CC DNA sequences have been isolated from Zea mays (corn), and the invention
CC also includes oligonucleotides AAC83114 - AAC83139 which are related to

the cell cycle polynucleotides. The cell cycle polynucleotide sequences are useful for producing transgenic plants such as maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet with increased levels of cell cycle gene activity, such as activity of cyclin and cyclin-dependent kinases. The DNA sequences are also useful as probes for detecting deficiencies in the level of mRNA in screening for desired transgenic plants, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detecting any number of allelic variants, orthologs or paralog of the gene, and site-directed mutagenesis in eukaryotic cells. The DNA sequences are also useful for recombinant expression of the encoded polypeptides and as immunogens for preparing and screening antibodies. A transgenic plant comprising an expression cassette including a cell cycle regulatory gene is useful for assaying enzyme agonists and antagonists, and as immunogens or antigens to obtain antibodies. The antibodies are useful in assaying expression levels of cell cycle regulatory proteins, for identifying and isolating nucleic acids from expression libraries, for identifying homologues of polypeptides from other species, and for purification of the proteins

Sequence 1930 BP; 518 A; 501 C; 545 G; 416 T; 0 U; 0 Other;

Sequence 1980 BP; 518 A; 501 C; 545 G; 416 T; 0 U; 0 Other;

Query Match 12.0%; Score 197; DB 3; Length 1980;
Best Local Similarity 54.9%; Pred. No. 1.8e-41;
Matches 464; Conservative 0; Mismatches 360; Indels 21; Gaps 3;

490	ATGGGTGCACAGAAACAAAGGACATATTGAACGAAGATGAATTGCTCATGATATTGAC	549
744	AAGGCTCCCTGTGGAAATCACTGATAAGACACGCGAAGTAGCAGTGAATCGAAGACATCGAC	803
550	AGTGACAGATCGGGGAACCGCTTGCTGCAACAGAAATATGTTAAAGAGCTTTACACCTTT	609
804	AAGTTGGAGCTCAACAATGAGCTCGAGTTGGGATACATTGAGGACATCTACAGCTTC	863
610	TACAGAGAAAATGAGGCTTAAGTTGTGAAGCCAGATTACATGTCCAGGCCAACAGAC	669
864	TACAAGATTGCTCAGACATGACAGACGCCCATG---TGAATTATAGACACCCCAAGTCGAG	920
670	ATAAACTCAAGATGAGAGCAATTTCTGATTGACTGGCTGATTGAGGTTCACTACAAGTTT	729
921	ATCAACCCCTAAGATGAGGGCTATCTGGCTGGTTGGATTAATTGAAGTACACCACAGTTTC	980
730	GAACTGATGATGAGACGCTCTTTCTTATGGTAAACATAATAGATAGATCTTTGGAAAAG	789
981	GAGCTGATGCGGAAACTCTCTACTTCTGACCATGTACATCATCAGTACCTCTCGCTG	1040
790	GAACTGGTTCCAGGAAGAGCTTACAACCTGGTTGGAGTCACAGCTATGCTGCTCGCTGT	849
1041	CAACCAGTCTCGGAAGGGAGCTCGAGCTGGTCGGTGTTCAGCTTATGCTGATCGCTGC	1100
850	AAATATGAGGAGGTATCTGTCCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTGC	909
1101	AAGTACGAGGAGATTGGGCCCCAGAGGTCGAACGATTTCACTTATATCAGACAGTGCA	1160
910	TACACAAAAGGGCAATTTTAGAANAAGGAAAGTTGATTTCTGACACCGTGCAGTTCAAC	969
1161	TACAGCAGGGAGAGATCCCTTTCCATGGGAAGGGAATCTGTAATAGCTGGAGTGGAAAC	1220
970	ATGCTGTGTTCCAAACACCTTATGTCTTCATCAAGAGGTTTCTGAAAGCTGCAG-----	1021
1221	CTCACTGTCCCTACAGTATACATGCTCTCTTGTTCGTTTCTGAAGCGGCGAGCCTTGGGC	1280
1022	-----ATGCAGATAAACAGCTTGAGCTAGCGTCAATTTTTATGCTGGAGCTCTCGTTGGTA	1077
1281	AACAAAGTTGAGAAAAGAGATGGAGAAATAGGTCCTTCTTCTTCGCTGAACCTGGCGCTGATG	1340
1078	GAATACCAAAATGCTGAATTAATCGGCCCTTCGCATCTGGCTGCTGTCGGGTTTATCTGCA	1137
1341	CAGTACGGCTTGGTACCGGGCTGCCCTTCGCTGGTCGCTCGTTGGTTGCTACGACGCC	1400
1138	CAGTGTGCTATCAATCGTTGCCAGCACTGGACAAAGGCTTCGAGTCTCATATA-----GC	1191
1401	AGGCTCACTCTCAAGAGGGCTCCCTCTGGAACCGACACCCCTCAAGACACCAACCGGGCTTC	1460

PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 14-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139753P.
PR 21-JUN-1999; 99US-0139817P.
PR 21-JUN-1999; 99US-0139889P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 23-JUN-1999; 99US-0140355P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140911P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142330P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145087P.
PR 23-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.

PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147453P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149388P.
PR 17-AUG-1999; 99US-0149417P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154019P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158023P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159337P.
PR 14-OCT-1999; 99US-0159382P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160982P.
PR 25-OCT-1999; 99US-0161403P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 11.7%; Score 191.8; DB 3; Length 1385;
Best Local Similarity 55.4%; Pred. No. 3.6e-40;

QY 776 GATCTTGGAAAGAGTGGTCCAGGAGAGCTAACACTGGTGGAGTCACAGCTA 835
 DB 751 GATTTTACAGGTTACAGCAGTTTCCCGAAGAGCTTCAATTAGTGGGATTAAGTCTC 810
 QY 836 TGCTGCTCGCTTGAATATAGAGAGGTATCTGTCTCCAGTGTGTGAGGACCTTGTGCTGA 895
 DB 811 TGCTCTGGCTTCCAGATGAGAGAGATGTTTCTCCAAATATTGAAGACTTTGTTTACA 870
 QY 896 TATCTGACCGTGCCTACACAAAAGGGCAATTTTGAATATGAAAGTTGATTTCTGAACA 955
 DB 871 TCACAGACAATGCTTATACCAAGTTTCCCAATCCGAGAAATGGAACCTCTAATTTTGAAG 930
 QY 956 CGCTGCAGTTCAACATGCTGTGTTCCACACCTTATGCTTCTCATGAAGAGTTTCTCAAAG 1015
 DB 931 AATTGAATTTGAGTTGGTTCGACCTTCCACTACACTTCTTAAGCGAGCATCAAAG 990
 QY 1016 CTGCAGATGAGATAAAGAGCTTGAAGTGTGATTTTCACTGCTGGAGCTCTGCTGG 1075
 DB 991 CCGGGAGGTTGATGTTGAACAGACACACTTTAGCCAAAGTATTTGATGGAGCTGACTCTCA 1050
 QY 1076 TAGAATACCAATGCTGAATTTATCGGCTTCCGATCTCGCTGCTGCTGC 1124
 DB 1051 TCGACTATGATGATGTCATTAATCACTCTTCTAAGTAGAGCAGCTGC 1099

RESULT 11
 AAH14263
 ID AAH14263 standard; cDNA; 1507 BP.
 XX AAH14263;
 AC AAH14263;
 XX AAH14263;
 DT. 26-JUN-2001 (first entry)
 XX Human cDNA sequence SEQ ID NO:11579.
 DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 KW Homo sapiens.
 OS Homo sapiens.
 XX EP1074617-A2.
 XX .07-FEB-2001.
 PD 28-JUN-2000; 2000EP-00116126.
 PF 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX (HELI-) HELIX RES INST.
 FA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 Claim 8; SEQ ID NO 11579; 2537pp + Sequence Listing; English.
 The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the polynucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH24446 to AAH58893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention
 XX Sequence 1507 BP; 427 A; 346 C; 337 G; 397 T; 0 U; 0 Other;
 SQ Query Match 9.8%; Score 150.2; DB 4; Length 1507;
 Best Local Similarity 55.7%; Pred. No. 9e-32;
 Matches 328; Conservative 0; Mismatches 258; Indels 3; Gaps 1;
 QY 536 TCATGATATTGACAGTGCAGACTCGGGAAACCCGCTTGTCTGCAACAGAAATATGTTAAAG 595
 DB 498 TCGAGACATTTGATTAACGAAGATTGGGAGAACCTCAGCTCTGCAGTACGTTAAGG 557
 QY 596 AGCTTTACACCTTTTACAGAGAAATAGAGCTTAAGGTTGTGTAGGCGCAGATACATGT 555
 DB 558 ATATCTATCAGTATCTCAGGCAGCTGGAGGTTTTCAGTCCATTAACCCACATTTCTTAG 617
 QY 656 CCAGCCACACAGACATAAATCAAGATGAGAGCAATTCGATTCAGCTGGCTGATGAGG 715
 DB 618 ATGG--AAAGATATAAATGAGCCATGCGTCCATCTAGTGGATTGGCTGTACAG 674
 QY 716 TTCCTACAGTTTGAAGTGTGATGAGAGCGCTCTTTCTTATGGTAAACATAATAGATA 775
 DB 675 TCCACTCCAAAGTTTAGGCTTCTGCAGGAGACTCTGTACATGTGCGTTGGCATTATGATC 734
 QY 776 GATTTTGGAAAAGAGTGGTTCAGAGAGAGCTCAACTGTTGAGTGCAGCTACAGCTA 835
 DB 735 GATTTTACAGGTTCCAGCCAGTTTCCCGAAGAGAGCTCAATTAGTGGGATTACTGCTC 794
 QY 836 TGCTGCTCGCTTGAATATAGAGAGGATCTGTTCCAGTTTGTGTTGAGGACCTTGTGCTGA 895
 DB 795 TGCTCTGGCTTCCAGTATGAGGAGATGTTTCTCCAAATATTGAAGACTTTGTTTACA 854
 QY 896 TATCTGACCGTGCCTACACAAAGGGCAATTTTGAATATGAAAGTTGATTTCTGAACA 955
 DB 855 TCACAGACAATGCTTATACCAAGTTCCCAATCCGAGAAATGGAACCTCTAATTTTGAAG 914
 QY 956 CGCTGCAGTTCAACATGCTGTGTTCCACACACCTTATGCTTTCATGAAGAGGTTTCTGAAG 1015
 DB 915 AATTGAATTTGAGTTGGTTCGACCTTGCACACTACTTCTTAAGGCGGAGCATCAAAG 974
 QY 1016 CTGCAGATGAGATAAAGAGCTTGAAGTGTGATGCTATTTTTCATGCTGGAGCTCTGCTGG 1075
 DB 975 CCGGGAGGTTGATGTTGAACAGCAGCAGCTTAGCCAAAGTATTTGATGAGCTGACTCTCA 1034
 QY 1076 TAGAATACCAATGCTGAATTTATCGGCTTCCGCTTCCATCTGGCTGCTGCTGC 1124
 DB 1035 TCGACTATGATGATGCTGATTAATCACTCTTCTTAAGTAGAGCAGCAGCTGC 1083

RESULT 12
 ACH03960
 ID ACH03960 standard; cDNA; 1532 BP.
 XX ACH03960;
 AC ACH03960;
 XX ACH03960;
 DT 26-SEP-2003 (first entry)
 XX Human cDNA differentially expressed in lung cancer #165.
 DE Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;
 KW

respiratory disorder; lung cancer; asthma; human.

Homo sapiens.

US2003065157-A1.

03-APR-2003.

04-APR-2002; 2002US-00116802.

04-APR-2001; 2001US-0281593P.

(LASEK) LASEK A W.

Lasek AW;

WPI; 2003-540803/51.

New combination comprising cDNAs that are differentially expressed in respiratory disorders, useful for diagnosing or treating respiratory disorders e.g., lung cancer, chronic obstructive pulmonary disease, emphysema or asthma.

Claim 1; Page; 39pp; English.

The invention relates to a combination comprising cDNAs or their complements that are differentially expressed in respiratory disorder. The combination is useful for preparing a composition for diagnosing or treating respiratory disorders e.g. lung cancer, chronic obstructive pulmonary disease, emphysema or asthma. The present sequence represents human cDNA differentially expressed during lung cancer

'Sequence 1532 BP; 433 A; 350 C; 347 G; 402 T; 0 U; 0 Other;

* Query Match 9.8%; Score 160.2; DB 8; Length 1532;

Best Local Similarity 55.7%; Pred. No. 9.1e-32; Indels 3; Gaps 1;

Matches 328; Conservative 0; Mismatches 258;

536 TCATGATATTGACGTGACACTCGGGAAACCGCTTCTGCAACAGAAATATGTTAAAG 595

518 TCAGGACATTGATACGAGATTGGAGAACCTCAGCTCTGCACTGACTACGTTAAGG 577

596 AGCTTTACCTTTTACAGAGAAATGAGCTAAGAGTTGTGTAAAGCCAGATACATCT 655

578 ATATCTATCATGATCTCAGGACGCTGGAGGTTTTCAGTCCATTAACCCACATTTCT 637

656 CCAGCCCAACAGACATATACTCAAGATGAGCAATTTCTGATTGCTGCTGATGAGG 715

638 ATGG---AAGAGATATAATGAGCGCATGCTGCCATCTAGTGGATTGCTGTACAAG 694

716 TTCACTACAAGTTTGAATGATGATGAGAGCGCTCTTTCTATGTTAAACATAATAGATA 775

695 TCCACTCCAAAGTTTAGGCTTCTGAGGAGACTCTGTACATGTCGTTGGCATTATGGATC 754

776 GATTCTTGGAAAGAGTGGTTCCAGGAGAGAGCTTACAACCTGGTTGGAGTCACAGCTA 835

755 GATTTTACAGGTTACCCAGCTTCCCGGAGAGAGCTTCAATAGTTGGATTACTGCTC 814

836 TGCTGCTCGTTGTAATATGAGAGGATCTCTGTTCCAGTTGTTAGGACCTTGCTGTA 895

815 TGCTCTTGGCTTCCAAATATGAGAGATGTTTCTCCAAATATGAGAGCTTTGTTTCA 874

896 TATCTGACCGTCCCTACACAAAGGCAATTTTAGAAATGGAAGTTGATCTGAACA 955

875 TCACAGACAATGCTTATACCGATTCCCAATCCGAGAAATGGAAGCTTAATTTGAAG 934

956 CGCTGCAAGTCAACATGCTTCTTCCAAACACTTATGCTTCAAGAGAGTTTCTGAAG 1015

935 AATTGAAATTTGAGTTGGTTCGACCTTTCGACCTACACTTCTTAAGCGCAGATCAAAAG 994

1016 CTGCAGATGACATAAAGAGCTTGAAGTCTAGCTGATTTTTCATGCTGAGCTCTGCTTG 1075

995 CCGGGAGGTTGATGTTGAACAGCACACTTTAGCCAAAGTATTTGATGAGCTGACTCTCA 1054

QY 1076 TAGAATACCAATGCTGAATTTATCGGCTTCCCATCTGCATCTGGCTGCTGCTGC 1124

Db 1055 TCGACTATGATATGCTGCAATTTATCATCTCTTAAGGTAGCAGCAGCTGC 1103

RESULT 13

AAV83711 standard; DNA; 1981 BP.

AAV83711;

05-MAR-1999 (first entry)

Nucleic acid encoding a cyclin related protein HCRP-2.

Human cyclin related protein; HCRP; HCRP-2; cancer; adenocarcinoma; leukemia; immune disorder; AIDS; asthma; developmental disorder; renal tubular acidosis; cerebral palsy; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 130..1326

FT /tag= a /product= "HCRP-2"

FT WO9855510-A2.

FT 10-DEC-1998.

PF 05-JUN-1998; 98WO-US011735.

PR 05-JUN-1997; 97US-00870143.

PA (INCY-) INCYTE PHARM INC.

PI Hillman JL, Corley NC, Guegler KJ, Cocks BG, Shah P;

DR WPI; 1999-045731/04.

DR P-PSDB; AAW87566.

Human cyclin related protein, HCRP - useful, e.g. to diagnose and treat cancer, immune disorders and developmental disorders and screen for antagonists used to treat cancer.

Claim 24; Fig 2A-F; 80pp; English.

The present sequence encodes a human cyclin related protein (HCRP) designated HCRP-2. HCRP proteins can be used to treat cancer e.g. adenocarcinoma, leukemia, etc. or immune disorders e.g. AIDS, asthma. They can also be used to treat developmental disorders, e.g. renal tubular acidosis, cerebral palsy. HCRP-2 was expressed in cancerous and foetal tissues, and increased expression with developmental disorders. HCRP with cancer and decreased expression with developmental disorders. HCRP can be used to screen for agonists (useful to treat conditions as above) or antagonists. It can be used to generate antibodies, useful as antagonists or to diagnose conditions characterised by HCRP expression and to monitor therapeutic interventions. Polynucleotides encoding HCRP can be used to detect polynucleotides encoding HCRP, e.g. to diagnose diseases relating to polypeptide expression or monitor HCRP regulation during therapeutic intervention. They are useful to produce complementary or antisense sequences for therapeutic administration to modulate or prevent HCRP expression e.g. to treat or prevent cancers as above

Sequence 1981 BP; 506 A; 504 C; 417 G; 546 T; 0 U; 8 Other;

Query Match 9.8%; Score 160.2; DB 2; Length 1981;

Best Local Similarity 55.7%; Pred. No. 1e-31; Indels 3; Gaps 1;

Matches 328; Conservative 0; Mismatches 258;

QY 536 TCATGATATTGACAGTGCAGACTCGGGAAACCGCTTGTGCAACAGATATGTTAAAG 595

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX Mus musculus.
OS WC0200189188-A2.
PN 22-NOV-2001.
PD 18-MAY-2001; 2001WO-JP004192.
XX PF 18-MAY-2000; 2000JP-00145977.
XX PR (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX PA Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX PI WPI; 2002-034733/04.
XX DR P-PSDB; ABB57124.
XX DR
XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX PT expression levels of particular genes defined in the specification or by
XX PT determining the expression profile of a gene group comprising these
XX PT genes.
XX PS Claim 2; Page 783-786; 2690pp; English.
XX PS
XX CC The present invention describes a method for examining ischaemic
XX CC conditions, comprising measuring the expression levels of particular
XX CC genes (I) in a test sample or determining the expression profile of a
XX CC gene group in the sample comprising genes selected from (I). The method
XX CC is useful for examining the ischaemic condition (e.g. compressive
XX CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
XX CC protein sequences in ABB57020 to ABB57374) or by determining the
XX CC expression profile of a gene group comprising these genes. The expression
XX CC levels or expression profiles produced by these genes are used as an
XX CC indicator when screening for ischaemic condition-improving drugs or
XX CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
XX CC primers for a mouse ischaemic condition related sequence, which are used
XX CC in the exemplification of the present invention
SQ Sequence 2308 BP; 631 A; 499 C; 517 G; 661 T; 0 U; 0 Other;

Query Match 9.5%; Score 155.6; DB 6; Length 2308;
Best Local Similarity 55.1%; Pred. No. 1.9e-30;
Matches 327; Conservative 0; Mismatches 284; Indels 3; Gaps 1;

QY 536 TCATGGATATTGACAGTCGAGACTCGGGGAACCCGGTTGCTGCAACAGAGATATGTTAAAG 595
DB 524 TGAGTGACGTAGACGCAGATGATGGGGCTGACCCAAACCTCTGTAGTGAATATGTGAAG 583
QY 596 AGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGAAGCCAGATTACATGT 655
DB 584 ATATCTATGCTTATCTCCGCAACTGGAGGAGAGAGAGTCACTTACCTCAATTAATACCTAC 643
QY 656 CCAGCCAAACAGACATAACTCAAAGATGAGAGCAATTCGATTGACTGGCTGATTGAGG 715
DB 644 AGGTCGTGAAG---TGACTCGAAACATGAGAGCTATCCTCATTTGACTGGCTAATACAGG 700
QY 716 TTCCTACAGATTTGAACTGATGATGAGAGCGCTCTTCTTATGTTGAACATATAGATA 775
DB 701 TTCAGATGAATTTAGGTCGCTTCAGGAGACCATGTACATGACTGTGTCTCATTATTGATC 760
QY 776 GATTCCTGGAAGGAAGTGGTTCCAGGAAAGAGCTACAACTGGTTGGAGTCACAGCTA 835
DB 761 GGTTCATCCAGACAGATTTGTGTGCCAAGAGAGATGCTACAGCTGTCGGTGAACGCCCA 820
QY 836 TGCTCTCGCTTGAATATGAGGAGGATCTGTTCCAGTTGTTGAGGACCTTGCTGTA 895
DB 821 TGTTTATTTGCAAGCAAAATATGAGGAGATGTACCCCTCCAGAAATAGGTGACTTCGCTTTG 880
QY 896 TATCTGACCGTGCCTTACACAAAAGGGCAAAATTTAGAAATGGAAGAGTTGATCTCTGAACA 955

DB 881 TGACTTAACACACGTACACTAAGCACACAGATCAGACAGATGGAGATGAAGATTTCTCAGAG 940
QY 956 CGTGCAGTTTCAACATGTCGTTCACACACCTTATGCTTTCATGAAGAGTTTCTGAAAG 1015
DB 941 TTTGAACTTTCAGCCTGGGTCGCCCTCTGCTCTGCACTTCTCCGTAGAGCATCTAAG 1000
QY 1016 CTGCAGATGCAGATAAAACAGCTTTGAGCTAGCGTCAATTTTCACTGCTGGAGCTCTGCTGG 1075
DB 1001 TCGGAGAGGTTGACGTCGAGCAGCACACTTTGGCCAAATACCTCATGGAGCTCTCCATGC 1060
QY 1076 TAGAATACCAATGCTGAATATATCGGCTTTCGATCTGCTGCTGCTGCTGCTGCTGCTGCT 1129
DB 1061 TGGACTCGGACATGGTGCATTTTGTCTCTCTCAAAATTCAGCTGGGGCTTTCT 1114

Search completed: March 20, 2004, 20:02:04
Job time : 679 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 19:36:30 ; Search time 131 Seconds
(without alignments)
6930.532 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1536
Sequence: 1 tcacggggtcttcctcgccg.....aaaaaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	223.4	13.7	274	4	US-09-313-294A-263	Sequence 263, App
2	160.2	9.8	1375	4	US-10-083-889-21	Sequence 21, Appl
3	160.2	9.8	1530	4	US-10-083-889-1	Sequence 1, Appl
4	155.4	9.5	1452	1	US-08-187-785-2	Sequence 2, Appl
5	155.4	9.5	1452	4	US-09-023-655-1048	Sequence 1048, Ap
6	153.8	9.4	1302	1	US-08-425-299A-1	Sequence 1, Appl
7	141.6	8.7	1336	4	US-10-083-889-25	Sequence 25, Appl
8	125.6	7.7	1634	2	US-08-460-895-1	Sequence 1, Appl
9	125.6	7.7	1634	2	US-09-210-889-1	Sequence 1, Appl
10	125.6	7.7	1649	2	US-08-692-787-8	Sequence 8, Appl
11	125.6	7.7	1649	3	US-09-097-139-8	Sequence 8, Appl
12	125.6	7.7	1649	4	US-09-023-655-1268	Sequence 1268, Ap
13	119.6	7.3	1752	1	US-08-463-090B-4	Sequence 4, Appl
14	111.6	6.8	826	3	US-09-337-171-12	Sequence 12, Appl
15	111.6	6.8	826	3	US-09-773-459-12	Sequence 12, Appl
16	97	5.9	333	4	US-09-023-655-64	Sequence 64, Appl
17	86.6	5.4	638	3	US-09-328-111-186	Sequence 186, App
18	86.8	5.3	1212	2	US-09-092-770-18	Sequence 18, Appl
19	86.8	5.3	1212	3	US-09-222-851-18	Sequence 18, Appl
20	85.6	5.2	1215	2	US-09-092-770-8	Sequence 8, Appl
21	85.6	5.2	1215	3	US-09-222-851-8	Sequence 8, Appl
22	72	4.4	1215	2	US-09-092-770-1	Sequence 1, Appl
23	72	4.4	1215	3	US-09-222-851-1	Sequence 1, Appl
24	71.4	4.4	1212	2	US-09-092-770-17	Sequence 17, Appl
25	71.4	4.4	1212	3	US-09-222-851-17	Sequence 17, Appl
26	69.8	4.3	1212	2	US-09-092-770-2	Sequence 2, Appl
27	69.8	4.3	1212	3	US-09-222-851-2	Sequence 2, Appl

28	64	3.9	1214	2	US-09-092-770-7	Sequence 7, Appl
29	64	3.9	1214	3	US-09-222-851-7	Sequence 7, Appl
30	59.8	3.7	273	4	US-09-313-294A-1848	Sequence 1848, Ap
C 31	58.4	3.6	532	4	US-09-389-681-432	Sequence 432, App
C 32	58.4	3.6	532	4	US-09-620-405B-432	Sequence 432, App
C 33	58.4	3.6	532	4	US-09-433-826B-432	Sequence 432, App
C 34	58.4	3.6	532	4	US-09-604-287A-432	Sequence 432, App
C 35	58.4	3.6	532	4	US-09-834-759-432	Sequence 432, App
36	58.2	3.6	1101	3	US-08-895-707-5	Sequence 5, Appl
37	58.2	3.6	1158	3	US-08-895-707-8	Sequence 8, Appl
38	58.2	3.6	1179	1	US-08-706-539-3	Sequence 3, Appl
39	58.2	3.6	1179	3	US-09-027-007-3	Sequence 3, Appl
40	58.2	3.6	1188	1	US-08-706-539-2	Sequence 2, Appl
41	58.2	3.6	1188	3	US-09-027-007-2	Sequence 2, Appl
42	58.2	3.6	1311	1	US-08-706-539-4	Sequence 4, Appl
43	58.2	3.6	1311	3	US-09-027-007-4	Sequence 4, Appl
44	58.2	3.6	1680	1	US-08-706-539-1	Sequence 1, Appl
45	58.2	3.6	1680	1	US-08-522-166-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-313-294A-263
; Sequence 263, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 263
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700548873H1
US-09-313-294A-263

Query Match	13.7%	Score	223.4	DB	4	Length	274
Best Local Similarity	93.5%	Pred. No.	1.6e-52				
Matches	244	Conservative	0	Mismatches	16	Indels	1
						Gaps	1
QY	627	TAAGAGTTCTGTAAAGCCAGATTACATGTCCAGCCAAACAGACATAAACTCAAAGATGAG	686				
DB	1	TAAGAGTTCTGTAAAGCCAGATTACATGTCCAGTCAGCAGATATATAATTCANAGATGAG	60				
QY	687	AGCAATTCCTGATGACTGGCTGATTGAGTTCACTACAGTTTGAATGATGATGATGAG	746				
DB	61	AGCAATTCCTGATGACTGGCTGATTGAGTTCACTACAGTTTGAATGATGATGATGAG	120				
QY	747	GCTCTTCTTATGTTAAACATATAGATAGATTCTTGGAAAGGAAGTGTTCCCAAGGAA	806				
DB	121	GCTATTTCTTACGTTAAACGTAATAGATAGATTCTTGGAAAGGAAGTGTTCCCAAGGAA	180				
QY	807	GAAGCTACAACTGGTTGGAGTCACAGCTATGCTGCTTCTTAATATGAGGAGTATC	866				
DB	181	GAAGCTACAACTGGTTGGAGTCACAGCTATGCTGCTTCTTGAATATGAGGAGTATC	239				
QY	867	TGTTCCAGTTGTTGAGGACCT	887				
DB	240	AGTTCCAGTTGTTGAGGACCT	260				

RESULT 2
US-10-083-889-21

; Sequence 21, Application US/10083889
; Patent No. 6573894
; GENERAL INFORMATION:
; APPLICANT: Zahner, Joseph E.
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
; FILE REFERENCE: 16850-7331
; CURRENT APPLICATION NUMBER: US/10/083,889
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/271,798
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 21
; LENGTH: 1375
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-083-889-21

Query Match 9.8%; Score 160.2; DB 4; Length 1375;
Best Local Similarity 55.7%; Pred. No. 1.6e-34;
Matches 328; Conservative 0; Mismatches 258; Indels 3; Gaps 1;

QY 536 TCATGGATATTCAGATGTCAGACTCGGGGAACCGCTTGTCTGCAACAGAAATATGTTAAAG 595
DB 528 TCGAGGACATTTGATAACCAAGATTGGGAGAACCCCTCAGCTCTGCAGTGACTACGTTAAAG 587
QY 596 AGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAAGCCAGATTACATGT 655
DB 588 ATATCTATCAGTATCTCAGGCAGCTGGAGGTTTTCAGTCCATTAACCCACATTTCTTAG 647
QY 656 CCAGCCACAGACATTAACCTCAAGATGAGAGCAATCTGATGCTGCTGCTGCTGCTGCTG 715
DB 648 ATGG---AAGAGATATAAATGAGCGCATGCGTCCATCTCTAGTGGATTTGGTGAAGA 704
QY 716 TTCCTACCAAGTTTGAATGATGATGAGAGCTCTTTCTTATGTTAAACATTAATAGATA 775
DB 705 TCCACTCCAAAGTTTAGGCTTCTGCAGGAGCTCTGTACATGTGCGTTGGCATTTATGATC 764
QY 776 GATCTTGGAAAGAGAGTGTTCAGAGGAAGAGCTACAACTGGTTGAGTGCAGCTA 835
DB 765 GATTTTACAGGTTTACAGCACTTCCCGGAAGAGCTTCAATAGTTGGATTTACTGCTC 824
QY 836 TGCTCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTCTGA 895
DB 825 TGCTCTCGCTTCCAGATATGAGGAGATGTTTCTCCAAATATGAGACTTTGTTTACA 884
QY 896 TATCTGACCGTCTACACAAAGGCAAAATTTAGAAATGGAAGTTGATCTCAACA 955
DB 885 TCACAGACAAATGCTTATACCAAGTTCCTCAATTCGAGAAATGGAACCTCTAAATTTGAAG 944
QY 956 CGCTGCAATTCACATGCTCTGTTCCAAACCTTATGTTCTCATGAAGAGGTTTCTGAAAG 1015
DB 945 AATTGAAATTTGAGTTGGTTCGACCTTGCACCTACACTTCTTAAGCGAGCATCAAAAG 1004
QY 1016 CTGCAGATGCAGATAACAGCTTGCAGCTAGGCTATGCTATTTTCATCTGCGAGCTGCTGG 1075
DB 1005 CCGGGAGGTTGATTTGAAACAGCACACTTTAGCCAAAGTATTTGATGGAGCTGACTCTCA 1064
QY 1076 TAGAATACCAATGCTGAATTCGCGCTTGCATCTGGCTGCTGCTGCTG 1124
DB 1065 TCGACTATGATATGTTGCTGATTTATCATCTCTTCAAGGTAGCAGAGCTGC 1113

RESULT 3
US-10-083-889-1
; Sequence 1, Application US/10083889
; Patent No. 6673894
; GENERAL INFORMATION:
; APPLICANT: Zahner, Joseph E.
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
; FILE REFERENCE: 16850-7331
; CURRENT APPLICATION NUMBER: US/10/083,889
; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: US 60/271,798
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Liu, J.H.
; AUTHORS: Wei, S.
; AUTHORS: Burnette, P.K.
; AUTHORS: Camero, A.M.
; AUTHORS: Hutton, M.
; AUTHORS: Djou, J.Y.
; TITLE: Functional association of TGF-beta receptor II with cyclin B
; JOURNAL: Oncogene
; VOLUME: 18
; ISSUE: 1
; PAGES: 269-275
; DATE: 1999-01-07
; DATABASE ACCESSION NUMBER: Genbank Accession No. 6673894 NM_004701
; DATABASE ENTRY DATE: 2000-11-01
; US-10-083-889-1

Query Match 9.8%; Score 160.2; DB 4; Length 1530;
Best Local Similarity 55.7%; Pred. No. 1.7e-34;
Matches 328; Conservative 0; Mismatches 258; Indels 3; Gaps 1;

QY 536 TCATGGATATTCAGATGTCAGACTCGGGGAACCGCTTGTCTGCAACAGAAATATGTTAAAG 595
DB 498 TCGAGGACATTTGATAACCAAGATTGGGAGAACCCCTCAGCTCTGCAGTGACTACGTTAAAG 557
QY 596 AGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAAGCCAGATTACATGT 655
DB 558 ATATCTATCAGTATCTCAGGCAGCTGGAGGTTTTCAGTCCATTAACCCACATTTCTTAG 617
QY 656 CCAGCCACAGACATTAACCTCAAGATGAGAGCAATCTGATGCTGCTGCTGCTGCTGCTG 715
DB 618 ATGG---AAGAGATATAAATGAGCGCATGCGTCCATCTCTAGTGGATTTGGTGAAGA 674
QY 716 TTCCTACCAAGTTTGAATGATGATGAGAGCTCTTTCTTATGTTAAACATTAATAGATA 775
DB 675 TCCACTCCAAAGTTTAGGCTTCTGCAGGAGCTCTGTACATGTGCGTTGGCATTTATGATC 734
QY 776 GATCTTGGAAAGAGAGTGTTCAGAGGAAGAGCTACAACTGGTTGAGTGCAGCTA 835
DB 735 GATTTTACAGGTTTACAGCACTTCCCGGAAGAGCTTCAATAGTTGGATTTACTGCTC 794
QY 836 TGCTCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTCTGA 895
DB 795 TGCTCTCGCTTCCAAAGTATGAGGAGATGTTTCTCCAAATATTAAGACTTTGTTTACA 854
QY 896 TATCTGACCGTCTACACAAAGGCAAAATTTAGAAATGGAAGTTGATCTCAACA 955
DB 855 TCACAGACAAATGCTTATACCAAGTTCCTCAATTCGAGAAATGGAACCTCTAAATTTGAAG 914
QY 956 CGCTGCAATTCACATGCTCTGTTCCAAACCTTATGTTCTCATGAAGAGGTTTCTGAAAG 1015
DB 915 AATTGAAATTTGAGTTGGTTCGACCTTGCACCTCTCTTAAAGGCGAGCATCAAAAG 974
QY 1016 CTGCAGATGCAGATAACAGCTTGCAGCTAGCTATTTTTCATGCTGAGAGCTGCTGCTGG 1075
DB 975 CCGGGAGGTTGATTTGAAACAGCACACTTTAGCCAAAGTATTTGATGGAGCTGACTCTCA 1034
QY 1076 TAGAATACCAATGCTGAATTTATGCGCTTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1124
DB 1035 TCGACTATGATATGTTGCTGATTTATCATCTCTTCAAGGTAGCAGAGCTGC 1083

RESULT 4
US-08-187-785-2
; Sequence 2, Application US/08187785

Mon Mar 22 09:47:00 2004

```

Patent No. 5756476
GENERAL INFORMATION:
APPLICANT: Epstein, Stephen
APPLICANT: Unger, Ellis
APPLICANT: Speir, Edith
TITLE OF INVENTION: Inhibition of No. 5756476-Transformed Cell
Proliferation Using Anti-Sense Oligonucleotides
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,785
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,415
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH001.001A
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human
IMMEDIATE SOURCE:
CLONE: Cyclin B1 cDNA clone
US-08-187-785-2

Query Match 9.5% Score 155.4; DB 1; Length 1452;
Best Local Similarity 54.7%; Pred. No. 3.6e-33;
Matches 331; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

QY 536 TCATGGATATGACAGTCGAGATCGGGGAACCCGCTTGTGCAACAGAAATATGTTAAG 595
DB 547 TAAATGATGTCGATGTCAGAGATGGAGCTGATCCAAACCTTTGTAGTGAATATGTAAG 606
QY 596 AGCTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAGCCAGATTACATGT 655
DB 607 ATATTTATGCTTTATCTGAGACACTTGGAGGAAGCAAGCAGTCACCAATACCTAC 666
QY 656 CCAGCCCAACAGACATAAATCAAGATGAGACAAATCTGTATGATGCTGCTGATTGAGG 715
DB 667 TGGTCGGGAAG--TCACTGGAACATGAGAGCCATCTTAATGACTGCTAGTACAGG 723
QY 716 TTCACTACAGTTGAACTGATGATGAGCGCTTTCTTTATGTTGTAACATATAGATA 775
DB 724 TTCAATGAATTCAGGTGTTGAGGAGACCATGTACATGATGCTCTCAATATTGATC 783
QY 776 GATTCTTGGAAAAGGAGTGGTTCCAAAGGAAGGCTACAACTGGTTGGAGTCACAGCTA 835
DB 784 GGTTCATCGAATAATTTGTGTGCCCAAGAGATGCTGCAGCTGGTTGGTGTCACTGCCA 843

```

```

QY 836 TGCTGCTCGCTTGAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGCTGA 895
DB 844 TGTTTATTCGACGAAATATGAAGAAATGTACCTCCAGAAATGGTGACTTGTCTTTG 903
QY 896 TATCTGACCGTGCCTACACAAAAGGCAATTTTAGAAATGGAAGTTGATTCGAACA 955
DB 904 TGACTGACAACTTATATCTAAGCAACCAATCAGACAGATGGAATGAAGATTCCTAAG 963
QY 956 CGCTGCAGTTCAACATGCTGTTTCCAAACACCTTATCTCTTCAAGAGAGTTTCTGAAG 1015
DB 964 CTTTAAACTTTGGTCTGGGTCGGCCTCTACCTTTGCACITTCCTCGGAGAGCATCTAAG 1023
QY 1016 CTGCAGATGCAATAAACAGCTTGAGCTAGCGTCATTTTCATGCTGGAGCTCTGCTCG 1075
DB 1024 TTGGAGAGGTTGATGTCGAGCAACATCTTTGGCCAAATACCTGTATGGAACCTAATGT 1083
QY 1076 TAGAATACCAAAATGCTGAATATTCGGCCTTTCGATCTGGCTGCTGGGTTTATFAC 1135
DB 1084 TGACTATGACATGGTGCACTTTCTCCCTCTCAATTCGACAGAGCTTTTGGCTTAG 1143
QY 1136 CACAG 1140
DB 1144 CACTG 1148

RESULT 5
US-09-023-655-1048
Sequence 1048, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1048:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g181243
US-09-023-655-1048

```

Query Match 9.5%; Score 155.4; DB 4; Length 1452;
Best Local Similarity 54.7%; Pred. No. 3.6e-33;
Matches 331; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

QY 536 TCATGGATATTCAGAGTGCAGACTCGGGGAACCCGCTTGTCTGCAACAGAAATATGTTAAAG 595
Db 547 TAAATGATGTGGATGCAGAGATGGAGCTGATCAAAACCTTTGTAGTGAATGTTGAAAG 606
QY 596 AGCTTTACACCTTTTACAGAGAAATGAGGCTAGAGTGTGTGAAGCCAGATTACATGT 655
Db 607 ATATTTATGCTTATCTGAGACAACTTGGAGAGAGCAGAGTCAACCAAAATACCTAC 666
QY 656 CCAGCCAAACAGACATAAATCAAGATGAGCAAAATTCGATGCTGCTGCTGATGAGG 715
Db 667 TGGGTTCGGGAAG---TCACTGGAACATGAGAGCCATCTTAATGCTGCTGCTAGTACAGG 723
QY 716 TTCACTCAAGTTTGAACCTGATGATGAGAGCGCTCTTCTTATGTTAAACATAATAGATA 775
Db 724 TTCAATGAATTCAGGTTGTTGAGAGAGCAATGATGATGCTGCTCAATATTGATC 783
QY 776 GATTCCTGGAAAGAAAGTGGTTCAGAGAGAGCTTCTTCTTATGTTAAACATAATAGATA 835
Db 784 GGTTCATGCAAAATTAATGTTGTGCCCCAAGAGATGCTGAGCTGGTGTGCTCACTGCCA 843
QY 836 TGCTGCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGA 895
Db 844 TGTATTGCAAGCAATATGAAGAAATGTACCTCCAGAAATTTGGTACTTTGCTTTG 903
QY 896 TATCTGACCGTGCCTACAAAAGGGGCAATTTTGAATGGAAGTTGATTTCTGAACA 955
Db 904 TGACTGCAACACTTATCTAAGCAACAAATCAGACAGATGGAATGGAAGATCTTAAGAG 963
QY 956 CGCTGCAAGTTCAACATGCTGTGTTCCAAACCTTATGTTCTATGAAGAGGTTTCTGAAG 1015
Db 964 CTTTAAACTTTGTCGGTGGCTCTACTTTGCACTTCTCTCGAGAGCATCTAAGA 1023
QY 1016 CTGAGATGAGATAAACACTTGAAGTACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1075
Db 1024 TTGAGAGGTTGATGTCGAGCAACACTTGTGCCCCAAATACCTGATGGAACATAATGT 1083
QY 1076 TAGAATACCAATGCTGAATATCGGCTTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1135
Db 1084 TGGACTATGACATGGTGCACCTTTCCTCTTCTCAAAATGCAAGAGAGCTTTTGTCTAG 1143
QY 1136 CACAG 1140
Db 1144 CACTG 1148

RESULT 6

US-08-425-299A-1
; Sequence 1, Application US/08425299A
; Patent No. 5726025
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: King, Randall W.
; APPLICANT: Peters, Jean-Michael
; TITLE OF INVENTION: Assay and Reagents for Detecting Inhibitors
; TITLE OF INVENTION: of Ubiquitin-dependent Degradation of
; TITLE OF INVENTION: Cell Cycle Regulatory Proteins
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,299A
FILING DATE: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1299
US-08-425-299A-1

Query Match 9.4%; Score 153.8; DB 1; Length 1302;
Best Local Similarity 54.5%; Pred. No. 9.5e-33;
Matches 330; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

QY 536 TCATGGATATTCAGAGTGCAGACTCGGGGAACCCGCTTGTCTGCAACAGAAATATGTTAAAG 595
Db 458 TAAATGATGTGGATGCAGAGATGGAGCTGATCCAAACCTTTGTAGTGAATATGTTAAAG 517
QY 596 AGCTTTACACCTTTTACAGAGAAATGAGGCTTAAAGTTGTGTAAGGCCAGATTACATGT 655
Db 518 ATATTTATGCTTATCTGAGACAACTTGAAGAGAGCAGAGCTCAGACCAAAATACCTAC 577
QY 656 CCAGCCAAACAGACATAAATCAAGATGAGAGCAATTTCTGATGCTGCTGCTGCTGCTGCTG 715
Db 578 TGGGTTCGGGAAG---TCACTGGAACATGAGAGCCATCTTAATGATGCTGCTGCTGCTGCTG 634
QY 716 TTCACTCAAGTTTGAACCTGATGGATGAGAGCGCTCTTCTTATGTTAAACATAATAGATA 775
Db 635 TTCAATGAAATTCAGGTTGTTGAGGAGAGCCATGATGATGCTGCTGCTGCTGCTGCTGCTG 694
QY 776 GATTCCTGGAAAGGAGTGGTTTCCAGAGAGAGCTACAACTGCTGAGAGTCAAGCTA 835
Db 695 GGTTCATGAGAAATTAATGTTGCCCCAAGAGATGCTGAGCTGGTGGTGTGCTGCTGCTGCTG 754
QY 836 TGCTGCTCGCTTGTAAATATGAGAGGATCTGTTTCCAGTTGTTGAGAGACCTTGTGCTGA 895
Db 755 TGTATTGCAAGCAAAATATGAAGAAATGTACCTCCAGAAATTTGTTGCTTTT 814
QY 896 TATCTGACCGTGCCTACACAAAGGGCAATTTTGAATGGAAGTTGATTTCTGACA 955
Db 815 TGACTGACCAACTTATATCTAAGCACCACCAATCAGACAGATGGAATGAAGATTCTTAAGAG 874
QY 956 CGCTGCAAGTTCAACATGCTGTCTTCCAAACACCTTATGCTTCTCATGAAGAGGTTTCTGAAG 1015
Db 875 CTTTAAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 934
QY 1016 CTGAGATGAGATAAACAGCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
Db 935 TTGAGAGGTTGATGTCGAGCAACATCTTTGGCCAAATACCTGATGGAATTAATCTATCT 994
QY 1076 TAGAATACCAATGCTGAAATATCGGCTTTCGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1135
Db 995 TGGACTATGACATGGTGCACCTTTCCTCTTCTCAAAATGCAAGAGAGCTTTTGTGCTTAG 1054
QY 1136 CACAG 1140
Db 1055 CACTG 1059

Db 1051 TTTCTGATCAGCAGCCTGCAAACTGCAAGTTGAAAGTTAGCAATGTTTTTGGGAGAA 1110
QY 1056 CTCCTGCTGGTAGAAT---ACCAATGCTGAATTATGCGCTTCGCACTCTGGCTGCTGCT 1122
Db 1111 TTAAGTTTGAATAGTGTGACCCATACCTCAAGTATTTGCCATCAGTTATGCTGGAGCT 1170
QY 1123 GCGGTTTATCTGCACTGCTGCTATCA 1150
Db 1171 GCCTTTTATGCACTCTACACAGTCA 1198

RESULT 9

US-09-210-889-1
; Sequence 1, Application US/09210889
; Patent No. 6103887
; GENERAL INFORMATION:
; APPLICANT: BRECHOT, Christian
; APPLICANT: WANG, Jian
; APPLICANT: CHENIVESSE, Xavier
; APPLICANT: HENGLEIN, Berthold
; APPLICANT: ZINDY, Fr d rique
; TITLE OF INVENTION: NEW HUMAN CYCLIN A COMPOSITIONS AND A
; TITLE OF INVENTION: PROCESS FOR THEIR PRODUCTION, THE CORRESPONDING NUCLEOTIDE SEQ
; TITLE OF INVENTION: A PROCESS AND AGENTS FOR CELL PROLIFERATION DETECTION OR DIAGN
; TITLE OF INVENTION: AND A PROCESS AND AGENTS FOR INHIBITING CELL PROLIFERATION.
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Larson and Taylor
; STREET: 727 Twenty-Third Street, South
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 500 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: MS-DOS version 3.0 or above
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/650, 805
; FILING DATE: 06-FEB-1991
; APPLICATION NUMBER: FR9001596
; FILING DATE: 12-FEB-1990
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: Human cyclin A
; LOCATION: coding sequence from base 97 to base 1392,
; LOCATION: coding for a protein of 432 amino acids.

US-09-210-889-1
Query Match 7.78; Score 125.6; DB 3; Length 1634;
Best Local Similarity 52.28; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;

QY 529 GAATGTCTCATGGATATTGACAGTGCAGACTCGGGGAACCCGCTTGCTGCAACAGAAATAT 588

Db 571 GACATGTCATTTGATTAGAGATGAAAGCCAGTGTATTAAGTACAGACTAC 630

QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTTAAGTGTGTAAAGCCAGAT 648

Db 631 CATGAGGATATTCACATACCTTAGGGAATGGAGGTTAAATGTAAACCTAAAGTGGCT 690
QY 649 TACATGTCAGCAACCAAGATGAGAGCAATTTCTGATTTGACTGGCTG 708
Db 691 TACATGAAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCCTCGTGGACTGGTTA 750
QY 709 ATTGAGGTTCACTACAAGTTTGAAGTGTGATGATGAGAGGCTCTTTCTTTATGTTAAACATA 768
Db 751 GTTGAAGTAGGAGAGAGATATTAATCTACAGATGAGAGCCCTGCAATTTGCTGTGAATAC 810
QY 769 ATAGATAGATTCTTGGAAGGAGAGTGGTTCCAGAGAGAGAGCTACAAGTGTGGAGTC 828
Db 811 ATTGATAGGTTCTGCTTCTTCCATGTCTGAGTGTGAGAGGAAACTTCAGCTTTGTTGGGCACT 870
QY 829 ACAGCTATGCTGCTGCTGTTGTAATATGAGGAGGATCTGTTCCAGTGTGTTGAGGACCTT 888
Db 871 GCTGCTATGCTGTTAGCTTCAAGTTTGAAGAAATATACCCCCAGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTCCCTACACAAAGGGGCAAAATTTAGAAATGGAAGTGTGATT 948
Db 931 GTGTACATTACAGATGATACCTACACCAAGAACTGTTCTGAGATGAGAGCATCTAGTT 990
QY 949 CTGAACAGCTGAGTTCAACATGCTGTTCCAAACACCTTATGCTTCAATGA---AGAGG 1005
Db 991 TTGAAGTCTTACTTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
QY 1006 TTTCTGAAAGCTGCAGATGCAAGTAAACAGCTTGAAGTGTGAGTGTGAGTGTGAGTGTGAG 1065
Db 1051 TTTCTGATCAGCAGCCTGCAAACTGCAAAAGTTGAAAGTTTGAAGTGTGAGTGTGAGTGT 1110
QY 1066 CTCGCTGCTGAGTAAT---ACCAAGTGTGAAATATGCGCTTCCGCTTCCGCTGCTGCTGCT 1122
Db 1111 TTAAGTTGATAGATGCTGACCCATACCTACCTCAAGTATTTGCCATCAGTTATTTGCTGGAGCT 1170
QY 1123 GCGGTTTATCTGCACTGCTGCTATCA 1150
Db 1171 GCCTTTTATGCACTCTACACAGTCA 1198

RESULT 10

US-08-692-787-8
; Sequence 8, Application US/08692787
; Patent No. 5882864
; GENERAL INFORMATION:
; APPLICANT: An, Gang
; APPLICANT: O'Hara, S. Mark
; APPLICANT: Ralph, David
; APPLICANT: Veltri, Robert
; TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
; TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/692,787
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Corger, Timothy S.
; REGISTRATION NUMBER: 38,414
; REFERENCE/DOCKET NUMBER: UROC:012
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-692-787-8

Query Match 7.7%; Score 125.6; DB 2; Length 1649;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;

QY 529 GAATTGCTCATGATTTGACATGTCAGAGTCCGGGAAACCCGCTTCTGCTCAACAGATAT 588
Db 582 GACATGTCATTTGATTTAGAGATGAAAGCCAGTGTATTAAGTACAGACTAC 641
QY 589 GTTAAAGAGCTTTACACATACCTTTAGGAAATGGAGTTAAATGTAACCTAAAGTGGT 701
Db 642 CATGAGATATTACACATACCTTTAGGAAATGGAGTTAAATGTAACCTAAAGTGGT 701
QY 649 TACATGTCAGCCAAAGACATAACTCAAGATGAGAGCAATTCGATTTGACTGGCTG 708
Db 702 TACATGAGAAACAGCCAGACATCACTACAGATGAGAGCTATCTCGTGGACTGGTA 761
QY 709 ATTGAGGTTTCACTACAGATTTGAACTGATGATGAGAGCTCTTTCTTATGTTAAACATA 768
Db 762 GTTGAAGTAGGAGAGATATAAACTACAGAAATGAGAGCTCTTTCTTATGTTAAACATA 821
QY 769 ATAGATAGATTTCTGAAAGAGAGTGGTTCAGAGAGAGAGTCTTCTGATGTTGAGATC 828
Db 822 ATTGATAGGTTCTGCTTCCATGTCAGTGTGAGAGAGAGAGTCTTCTGATGTTGAGATC 881
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGGAGGATCTGTTCCAGTTGTTGAGAGCTT 888
Db 882 GCTGCTATGCTGTTAGCTTCAAAAGTTTGAAGAAATATACCCCCAGAGAGTACAGAGTT 941
QY 889 GTGCTGATATGTCAGCTGCTTACATGCTGTTCCACACCTTATGTTCTTATGTTAAACATA 948
Db 942 GTGTACATTTACAGATGATACCTTACCAAGAAACAGTCTTGAAGATGAGAGCTATGAT 1001
QY 949 CTGAACAGCTGAGATGAGATTAACAGCTTGAAGAGTGTGAAAGTTTGAAGAGTGTG 1005
Db 1002 TTGAAGTCTTACITTTGACITTAGCTGCTCCACAGTAAATCAGTTTCTTACCAATAC 1061
QY 1006 TTTCTGAAAGCTGAGATGAGATTAACAGCTTGAAGTGTGAGTGTGAGTGTGAGTGTGAG 1065
Db 1062 TTTCTGCAATCAGCAGCTGCAAACTGCAAAAGTTTGAAGAGTGTGAGTGTGAGTGTGAG 1121
QY 1123 GCGGTTTATCTGACAGTGTGCTATCA 1150
Db 1182 GCCTTTCAATTAGCACTTACACAGTCA 1209

RESULT 11

US-09-097-199-8
Sequence 8, Application US/09097199
Patent No. 6218529
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: Ralph, David
APPLICANT: Velti, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-097-199-8

Query Match 7.7%; Score 125.6; DB 3; Length 1649;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;

QY 529 GAATTGCTCATGATTTGACATGTCAGAGTCCGGGAAACCCGCTTCTGCTCAACAGATAT 588
Db 582 GACATGTCATTTGATTTAGAGATGAAAGCCAGTGTATTAAGTACAGACTAC 641
QY 589 GTTAAAGAGCTTTACACATACCTTTAGGAAATGGAGTTAAATGTAACCTAAAGTGGT 701
Db 642 CATGAGATATTACACATACCTTTAGGAAATGGAGTTAAATGTAACCTAAAGTGGT 701
QY 649 TACATGTCAGCCAAAGACATAACTCAAGATGAGAGCAATTCGATTTGACTGGCTG 708
Db 702 TACATGAGAAACAGCCAGACATCACTACAGATGAGAGCTATCTCGTGGACTGGTA 761
QY 709 ATTGAGGTTTCACTACAGATTTGAACTGATGATGAGAGCTCTTTCTTATGTTAAACATA 768
Db 762 GTTGAAGTAGGAGAGATATAAACTACAGAAATGAGAGCTCTTTCTTATGTTAAACATA 821
QY 769 ATAGATAGATTTCTGAAAGAGAGTGGTTCAGAGAGAGAGTCTTCTGATGTTGAGATC 828
Db 822 ATTGATAGGTTCTGCTTCCATGTCAGTGTGAGAGAGAGTCTTCTGATGTTGAGATC 881
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGGAGGATCTGTTCCAGTTGTTGAGAGCTT 888
Db 882 GCTGCTATGCTGTTAGCTTCAAAAGTTTGAAGAAATATACCCCCAGAGAGTACAGAGTT 941
QY 889 GTGCTGATATGTCAGCTGCTTACATGCTGTTCCACACCTTATGTTCTTATGTTAAACATA 948
Db 942 GTGTACATTTACAGATGATACCTTACCAAGAAACAGTCTTGAAGATGAGAGCTATGAT 1001
QY 949 CTGAACAGCTGAGATGAGATTAACAGCTTGAAGAGTGTGAAAGTTTGAAGAGTGTG 1005
Db 1002 TTGAAGTCTTACITTTGACITTAGCTGCTCCACAGTAAATCAGTTTCTTACCAATAC 1061
QY 1006 TTTCTGAAAGCTGAGATGAGATTAACAGCTTGAAGTGTGAGTGTGAGTGTGAGTGTGAG 1065
Db 1062 TTTCTGCAATCAGCAGCTGCAAACTGCAAAAGTTTGAAGAGTGTGAGTGTGAGTGTGAG 1121
QY 1066 CTCTGCTTGTGAGAT---ACCAATGCTGAATTTAGGCTTGGCTTGGCTGCTGCT 1122

Db 1122 TTAAGTTGATAGTCTGACCATACCTCAAGTATTGGCCATCAGTTATTGCTGGAGCT 1181
Qy 1123 GCGGTTTATCTGACAGAGTGTGCTATCA 1150
Db 1182 GCCTTTCAATTAGCACTCTACACAGTCA 1209

RESULT 12

US-09-023-655-1268
; Sequence 1268, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1268:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1649 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 930306
US-09-023-655-1268

Query Match 7%; Score 125.6; DB 4; Length 1649;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
Qy 529 GAATGCTCATGATATTGACAGTGCAGACTCGGGGAACCCCGTTGCTGCAACAGAAATAT 588
Db 582 GACATGCTCAATTGTTATGAGATGAAAGCCAGTGAGTGTAAATGAAGTACCAGACTAC 641
Qy 589 GTTAAAGAGCTTTACACCTTTTACAGAAATGAGCTTAAGATTGTGTAAGCCAGAT 648
Db 642 CATGAGGATTTACACATACCTTAGGGAATGAGGTTAAATGAAACCTTAAGTGGGT 701
Qy 649 TACATGTCGACCAACAGACATAAACTCAAGATGAGAGCAATTTCAATTGACTGGCTG 708
Db 702 TACATGAAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCTCTGCTGGAGTTA 761

Qy 709 ATTGAGTTCTACTACAAGTTTGAACCTGATGATGAGAGCGCTCTTCTTATATGTTAAACATA 768
Db 762 GTTGAAGTAGGAGAGAAATATAAACTACAGAAATGAGACCCCTGCAATTTGGCTGTGAATAC 821
Qy 769 ATAGATAGATTCTTGGAAAAGGAAGTGTTCCTCAAGGAAGAGCTACAACTGGTTGGAGTC 828
Db 822 ATTGATAGTTCTCTCTCTCCATGCTGCTGAGAGGAAACCTCAGCTTGTGGGCACT 881
Qy 829 ACAGCTATGCTGCTGCTCTGTTGTAATATAGAGAGATCTGTTCCAGTTGTTGAGGACCTT 888
Db 882 GCTGCTATGCTGTTAGCTCTCAAGTTTGAAGAAATATACCCCCCAGAGTAGCAGAGTTT 941
Qy 889 GTGCTGATATCTGACCGTCTACACAAAAGGGCAAAATTTAGAAATGGAAGAAATTTGATT 948
Db 942 GTGTACATTACAGATGATACCTACACCAAGAAACAAGTCTGAGATGAGAGCACTAGTT 1001
Qy 949 CTGACACGCTGCTGCTCAACATGCTGTTCTGTTCCACACCTTATGCTTCTATGA---AGAGG 1005
Db 1002 TTGAAGTCTTACTTTTGTAGCTTGTCTCCACAGTAATCAGTTTCTTACCCATAC 1061
Qy 1006 TTTCTGAAAGCTGCAGATGCAGATAAAGCTGAGCTAGCGTCAATTTTTCATGCTGGAG 1065
Db 1062 TTTCTGATCAGCAGCTGCAAACTGCAAAAGTTGAAAGTTTAGCAATGTTTTTGGGAGAA 1121
Qy 1066 CTCTGCTTGTAGAT---ACAAATGCTGAATATCGGCTTGGCATCTGGCTGCTGCT 1122
Db 1122 TTAAGTTTGAATAGATGCTGACCCATACCTCAAGTATTGTCATGTTTCTTGGAGCT 1181
Qy 1123 GCGGTTTATCTGACAGCTGCTGCTATCA 1150
Db 1182 GCCTTTTATTAGCACTCTACACAGTCA 1209

RESULT 13

US-08-463-090B-4
; Sequence 4, Application US/08463090B
; Patent No. 5801015
; GENERAL INFORMATION:
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Guilio
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
; TITLE OF INVENTION: Human Pathogens, and Uses Related Thereto
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,090B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV032.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear

```
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 184...1659
US-08-463-090B-4

Query Match 7.3%; Score 119.6; DB 1; Length 1752;
Best Local Similarity 50.0%; Pred. No. 3.7e-23;
Matches 299; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

QY 540 GGATATTGACAGTCAGACTCGGGAAACCGCTTGTGCGAACAGATATGTTAAAGAGCT 599
Db 750 GGATTTGGATGACAGAGATATGACGACCAATTAATGGTTAGTCAATATGTTAAACGAAT 809
QY 600 TTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAGCGCAGATACATGTCAG 659
Db 810 ATTTTCGTACTATTACGATTTAGAAACACGAAATTTACCTGATCCGCAATATCTTTCAA 869
QY 660 CCAACAGACATAAATCAAGATGAGAGCAATTTCTGATTTGATGCTGGCTGATGAGGTTCA 719
Db 870 ACAACATTTGTTAAACCAAGATGAGATCGATATGTTGTTGATTTGGCTTTGTTGAAATGCA 929
QY 720 CTACAGTTTGAATCTGATGAGAGCGCTCTTTCTTTATGTAATAACATAATAGATGATT 779
Db 930 TTTAAATTTCAAGTTTATCTGATATCACATTTTTCGCGAGTCAATGTAATGATGATT 989
QY 780 CTTGGAAGAGGAGTGTTCAGAGGAAGAGCTACAACTGGTTGGAGTCAAGCTATGCT 839
Db 990 CATGCTCTTGAAGTGTTCAGATAGATAAATTAACAATTAATGCTACAGCAGCTTTATT 1049
QY 840 GCTGCTGTAAATATGAGGAGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATC 899
Db 1050 TACTGCTGCCAAAATGAAGAGTATTTCTCCCTGTTTAAATATGATATTTTAC 1109
QY 900 TGACCGTCCCTACACAAAGGCGCAATTTTGAATGAAAGTTGATTCTGAACACGCT 959
Db 1110 TGATGTTTCATATCTCCAGAGAGTGTGTAAGAGCAAAATACATGCTTACCATTT 1169
QY 960 CGAGTTCAACATGCTGTTCCACACCTTATGTTCTCATGAGAGGTTCTGGAAGCTGC 1019
Db 1170 TAACCTTGAATTTGAATTAACCCCAATCCAAATGAAATTTCTTGAGAAGAAATTTAAAGCTGA 1229
QY 1020 AGATCGATATAACAGCTTGAGCTAGCTGCTATTTTTCATGCTGGAGCTGCTGTTGTAGA 1079
Db 1230 TGATATGATGCTCAATCAAGACGCTAGGAATAATCTTTTGAATCACTATAGTTGA 1289
QY 1080 ATACCAATGCTGAATTAATGCGCTTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 1137
Db 1290 TTACAAATTTATGTTGATGAGACCATCTTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 1347

RESULT 14
US-09-337-171-12
; Sequence 12, Application US/09337171
; Patent No. 6262249
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Giulia C
; TITLE OF INVENTION: PANCREATIC CANCER GENES
; FILE REFERENCE: 200130.454
; CURRENT APPLICATION NUMBER: US/09/337,171
; CURRENT FILING DATE: 1999-06-21
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-337-171-12

Query Match 6.8%; Score 111.6; DB 3; Length 826;
Best Local Similarity 55.0%; Pred. No. 4.1e-21;
Matches 219; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 727 TTTGAACTGATGATGAGAGCGCTCTTTCTTATGTTAAACATAATAGATAGATTCTTGGAA 786
Db 1 TTTAGGCTTCTGAGGGGACTCTGTACATGTGCGTTGGCAATTATGGATCGATTTTACAG 60
QY 787 AAGGAAGTGTTCAGAGGAAGCTACAACTGGTTGGAGTCAAGCTATGCTGCTGCT 846
Db 61 GTTCAGCCAGTTTCCCGGAAGAAGCTTCAATTTAGTTGGGATTTACTGCTCTTGGCC 120
QY 847 TGTAAATATGAGGAGTATCTGTTCCAGTTTGTGAGGACCTTGTGCTGATATCTGACCGT 906
Db 121 TCCAAGTATGAGGAGATGTTTCTCCAAATATTGAAGACTTTGTTTACATCACAGACAA 180
QY 907 GCCTACACAAAAGGGCAAAATTTTAGAAATGGAAGAGTTGATTTCTGAAACCGTGCAGTTTC 966
Db 181 GCTTATACCAAGTTCCCAATCCGAGAAATGGAATCTTAATTTTGAAGAAATCGAAATTT 240
QY 967 AACATGCTGTTCCACACCTTATGCTTTCATGAGAGAGGTTTCTGAAAGCTGCAGATGCA 1026
Db 241 GAGTTGGTTCGACCCCTTCCCACTACATCTTTAAGGCGAGCATCAAAAGCCGGGAGGTT 300
QY 1027 GATAAACAGCTTGAGCTAGCTGATCTATTTTCACTGTTGGAGCTGCTGTTGGTAGMATACCAA 1086
Db 301 GATGTTGAACAGCACACTTTAGCCAAATTTGATGGAGCTGACTCTCATCGACTATGAT 360
QY 1087 ATGCTGAATTAATCGCCCTTCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1124
Db 361 ATGCTGAATTAATCATCTCTTCTTAAGGTAGCAGCAGCTGC 398

RESULT 15
US-09-773-459-12
; Sequence 12, Application US/09773459
; Patent No. 6664054
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Giulia C
; TITLE OF INVENTION: PANCREATIC CANCER GENES
; FILE REFERENCE: 200130.454
; CURRENT APPLICATION NUMBER: US/09/773,459
; CURRENT FILING DATE: 2001-01-31
; PRIOR FILING DATE: US 09/337,171
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-773-459-12

Query Match 6.8%; Score 111.6; DB 4; Length 826;
Best Local Similarity 55.0%; Pred. No. 4.1e-21;
Matches 219; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 727 TTTGAACTGATGATGAGAGCGCTCTTTCTTATGTTAAACATAATAGATAGATTCTTGGAA 786
Db 1 TTTAGGCTTCTGAGGGGACTCTGTACATGTGCGTTGGCAATTATGGATCGATTTTACAG 60
QY 787 AAGGAAGTGTTCAGAGGAAGCTACAACTGGTTGGAGTCAAGCTATGCTGCTGCT 846
Db 61 GTTCAGCCAGTTTCCCGGAAGAAGCTTCAATTTAGTTGGGATTTACTGCTCTTGGCC 120
QY 847 TGTAAATATGAGGAGTATCTGTTCCAGTTTGTGAGGACCTTGTGCTGATATCTGACCGT 906
Db 121 TCCAAGTATGAGGAGATGTTTCTCCAAATATTGAAGACTTTGTTTACATCACAGACAA 180
QY 907 GCCTACACAAAAGGGCAAAATTTTAGAAATGGAAGAGTTGATTTCTGAAACCGTGCAGTTTC 966
Db 181 GCTTATACCAAGTTCCCAATCCGAGAAATGGAATCTTAATTTTGAAGAAATCGAAATTT 240
QY 967 AACATGCTGTTCCACACCTTATGCTTTCATGAGAGAGGTTTCTGAAAGCTGCAGATGCA 1026
Db 241 GAGTTGGTTCGACCCCTTCCCACTACATCTTCTTAAGGTAGCAGCAGCTGC 398
```

Mon Mar 22 09:47:00 2004

Qy	1027	GATAAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAATACCAA	1086
Db	301	GATGTTGAACAGCACACTTTAGCCCAAGTATTTGATGGAGCTGACTCTCATCGACTATGAT	360
Qy	1087	ATGCTGAATTATCGGCCCTTCGCATCTGGCTGCTGCTGC	1124
Db	361	ATGGTGCATTATCATCCTTCTAAGGTAGCAGCAGCTGC	398

Search completed: March 20, 2004, 23:05:47
Job time : 134 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 20, 2004, 19:50:55 ; Search time 585 Seconds
(without alignments)
10344.983 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1636
Sequence: 1 tcaagggtctctccgtccg.....aaaaaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubna/FCN_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubna/FCN_PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1634	98.9	1636	10	US-09-496-444-1
2	1610	98.4	1699	15	US-10-310-154-50
3	702.2	42.9	1611	15	US-10-310-154-46
4	400.6	24.5	1793	15	US-10-310-154-44
5	388.8	23.8	1896	12	US-10-424-599-4753
6	355.4	21.7	1750	15	US-10-310-154-61
7	342.4	20.9	1281	15	US-10-260-238-497
8	243.8	14.9	1751	15	US-10-310-154-51
9	228.6	14.0	1141	12	US-10-424-599-118953
10	228.6	14.0	1384	15	US-10-260-238-1251
11	220.6	13.5	1944	12	US-10-424-599-103481
12	215.4	13.2	1816	12	US-10-424-599-118855
13	214.6	13.1	1338	9	US-09-938-842A-789
14	214.6	13.1	1338	11	US-09-938-842A-789
15	212.8	13.0	1850	15	US-10-310-154-52

16	212.2	13.0	715	12	US-10-424-599-24154
17	211.2	12.9	1086	12	US-10-425-114-17906
18	195.6	12.0	605	12	US-10-424-599-98711
19	173.2	10.6	1879	15	US-10-310-154-56
20	161.4	9.9	1553	9	US-09-925-301-305
21	157	9.6	1197	10	US-09-994-412-2
22	155.4	9.5	1452	9	US-09-954-456-695
23	155.4	9.5	1452	9	US-09-954-456-1133
24	155.4	9.5	1452	9	US-09-880-107-2308
25	155.4	9.5	1452	9	US-09-967-768A-145
26	155.4	9.5	1452	9	US-09-954-531-147
27	155.4	9.5	1452	9	US-09-292-758-27
28	155.4	9.5	1452	10	US-09-873-367C-1008
29	155.4	9.5	1452	14	US-10-171-581-136
30	155.4	9.5	1570	13	US-10-098-841-236
31	152	9.3	1278	14	US-10-128-714-2013
32	152	9.3	1347	14	US-10-128-714-1013
33	152	9.3	1464	14	US-10-128-714-7013
34	152	9.3	1577	14	US-10-128-714-6013
35	152	9.3	3347	14	US-10-128-714-13
36	152	9.3	3577	14	US-10-128-714-5013
37	149.2	9.1	873	12	US-10-424-599-52554
38	139.6	8.5	1905	12	US-10-425-114-13500
39	134.2	8.2	1539	15	US-10-369-493-27403
40	129.4	7.9	1247	15	US-10-085-198-109
41	127.2	7.8	1446	15	US-10-369-493-26031
42	127.2	7.8	1446	15	US-10-369-493-26040
43	125.6	7.7	1649	10	US-09-974-546-8
44	125.6	7.7	2504	13	US-10-108-605-246
45	125.6	7.7	3740	9	US-09-925-300-345

ALIGNMENTS

RESULT 1
US-09-496-444-1
; Sequence 1, Application US/09496444
; Publication No. US20030041343A1
; GENERAL INFORMATION:
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm William J.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Bailey, Matthew A.
; TITLE OF INVENTION: Cell Cycle Polynucleotide, Polypeptide,
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1109
; CURRENT APPLICATION NUMBER: US/09/496,444
; CURRENT FILING DATE: 2000-02-02
; EARLIER APPLICATION NUMBER: US 60/119,857
; EARLIER FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: US 60/101,551
; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: US 09/398,858
; EARLIER FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: US 09/257,131
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)...(1381)
; NAME/KEY: misc feature
; LOCATION: (1)...(1636)
; OTHER INFORMATION: n = A,T,C or G
US-09-496-444-1

Query Match 99.9%; Score 1634; DB 10; Length 1636;
Best Local Similarity 100.0%; Pred. No. 0;

QY 1128 TTATATGTCACAGTGTGCTATCAATCGTTGTCACAGCTGGACAAAGGTCTGGAGTCTCA 1187
Db 1075 TTACACAGCACAATGTGCTCTCACTGTTGCCAGCAGTGGACAAAGACCTGGCAACTACA 1134
QY 1168 TAGCAGATACACTAGCGACCAACTCTGGAGTGTCTCGAGGATGATGTAGATTTCACCA 1247
Db 1135 TAGTAGATATACCGAGAGCAGCTCTTGAGTGTCTTAGATGATGTAGATTTCACCA 1194
QY 1248 GAAGCTGGAAACCAAGTACCTCTGGCGTGCACAGGAAGTACAGTACCTACAGTTTCGG 1307
Db 1195 GAAGCGGAGCAGCAGCAAGCTCACCGGCTGCACCGGAATACACAGTACCTCAAGTTTGG 1254
QY 1308 TTGGTGGCCAGATTTTGGCTGGCGAGTCTCTGGAGTGTCTGGAGTGTGGAG--GGACACCGCT 1365
Db 1255 GTGTGACGCCAAACGAGCCTGTCTCTTCTGCTTGAGTCAGGACAGCAGGTTTCA 1314
QY 1366 CTTTCAGTGAACACTAGTGAATGACCTTCAACTGGGTGGATTTTAAAGTT 1422
Db 1315 CTTTCAGAGCAGCCTTGTGTAATGATCTATCCCTGGATAGATTTTAACTT 1371

RESULT 4

US-10-310-154-44

; Sequence 44, Application US/10310154

; Publication No. US20030233670A1

; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; APPLICANT: Chomet, Paul S.

; APPLICANT: Adams, Thomas H

; APPLICANT: Ruff, Thomas G.

; APPLICANT: Agarwal, Aneeta K.

; APPLICANT: Ahrens, Jeffrey E.

; APPLICANT: Ball, James A.

; APPLICANT: Banu, G.

; APPLICANT: Bell, Erin

; APPLICANT: Boddupalli, Raghava

; APPLICANT: Deikman, Jill

; APPLICANT: Deng, Mollan

; APPLICANT: Dong, Jinzhao

; APPLICANT: Duff, Stephen M.

; APPLICANT: Galligan, Meghan M.

; APPLICANT: Hinchey, Brenda S.

; APPLICANT: Huang, Shishui

; APPLICANT: Johnson, G. Richard

; APPLICANT: Jung, Vincent

; APPLICANT: Kretzmer, Keith A

; APPLICANT: Laccetti, Lucille B.

; APPLICANT: Lai, Chao-Qiang

; APPLICANT: Lee, Gary

; APPLICANT: Lin, Jie-yi

; APPLICANT: Liu, Jingdong

; APPLICANT: Lu, Bin

; APPLICANT: Luethy, Michael M.

; APPLICANT: Lund, Adrian

; APPLICANT: Madson, Linda L.

; APPLICANT: Malloy, Kathleen A.

; APPLICANT: McKiel, Christine L.

; APPLICANT: Miller, Philip W.

; APPLICANT: Padmavathi, Manchikanti

; APPLICANT: Parnell, Laurence D.

; APPLICANT: Start, William G.

; APPLICANT: Tennesen, Dan

; APPLICANT: Vidya, K.R.

; APPLICANT: Wang, Haiyun

; APPLICANT: Xin, Zhanguo

; APPLICANT: Xu, Nanfei

; APPLICANT: Yang, Chunzhi

; APPLICANT: Zeng, Xiaoping

; APPLICANT: Zhang, Qiang

; APPLICANT: Zhao, Vajuan

; APPLICANT: Zhou, Li

; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants

; FILE REFERENCE: 38-15(52796)B

; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 44
; LENGTH: 1793
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)...(1407)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1793)
; OTHER INFORMATION: unsure at all n locations
US-10-310-154-44

Query Match 24.5%; Score 400.6; DB 15; Length 1793;

Best Local Similarity 68.5%; Pred No. 3.2e-109; Indels 0; Gaps 0;

Matches 553; Conservative 0; Mismatches 254; Indels 0; Gaps 0;

QY 541 GATATTGACAGTCGACAGCTCGGGAAACCCGCTTGTGCAACAGATATGTTAAAGAGTT 600

Db 586 GATATTGACAGCTGTGATGCAATAAATCTCCCTTGCAGTAGTGAATATGTTGATGAAT 645

QY 601 TACACCTTTTACAGAGAAATGAGGCTTAAGAGTTGTGTAAGGCCAGATTACATGTCACG 660

Db 646 TACAGCTTCTACAGAGGAGTGAGGTTTGTGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 705

QY 661 CAACAGACATAAATCAAGATGAGCAANTTCTGATGAGTGTGCTGATGAGTTGCTAC 720

Db 706 CAAATGACATAAATGAGAAGATGCGCGCATCTCATCGATTGCTGATAGAGTGCAT 765

QY 721 TACAGTTTGAAGTGTGATGAGAGCGCTCTTCTTATGTTAAACATATAGATATTC 780

Db 766 TACAAGTTAGAGCTATTGATGAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 825

QY 781 TTGGAAAAGGAAGTGGTTCCAAAGGAAGAGCTCAACACTGGTTGGAGTCAAGCTATGCTG 840

Db 826 TTGGCTCGGAAAATGTGGTGCAGAAAGCTTCAGTTGGTTGGCTGACTGCCATGCTG 885

QY 841 CTCGCTTGAATATGAGAGGATATCTGTTCAGTTGTGAGGACCTTGTGCTGATATCT 900

Db 886 CTCGCTTGAAGTATGAAGAGTGTCTGTGTAGTGAGGATCTTATCTTAATCTGC 945

QY 901 GACCGTCTTACACAAAAGGCAAAATTTAGAAAATGGAAAAGTTGATCTGAACACGCTG 960

Db 946 GACCGGCTTACACAGAACAGATATCTCGAAATGGAGAGGATGATTGTAACACTCTT 1005

QY 961 CAGTTCAACATGCTGTTCCAAACACCTTATGCTTTCATGAAGAGGTTTCTGAAGTGA 1020

Db 1006 CAGTTTGATATGTAGTTCCAACTCCATCTCTTTTCATGAAGGTTTCTCAAGGCTGA 1065

QY 1021 GATGCAGATAAAGAGCTTTCAGCTAGGCTAGGCTATTTTCATGCTGGAGTCTGCTGGTAGAA 1080

Db 1066 CAATCTGACAGAGAGTTTGAAGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1125

QY 1081 TACAAAATGCTGAATATTCGGCTTTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

Db 1126 TATGAGATGCTCAAAATTCAGAGCGCTCAATGCTGGGGCTGCTGCCATCTACATGCTGCT 1185

QY 1141 TGTGCTTCAATCGTTGCCAGCAGCTGGACAAAGGCTGCGAGTCTCATAGCAGATACACT 1200

Db 1186 TGCACCAATTAATGGTTCAAGTCTTGAACAAATGCTGTGAGCTGATACAAATACTCT 1245

QY 1201 AGCGACCAACTCTCGAGTGTCTCGAGGATGATGTTGATGATGATGATGATGATGATGAT 1260

Db 1246 GAAGAACAGCTGATGAGTGTCTCCAGATGATGTTGAGTGTCTCCACCAAAAGCAGGACAT 1305

QY 1261 AGTAAGCTCACTGGCTGCGACAGGAGTACAGTACTCAAGTTCGGTTGCGTGGCCAG 1320

Db	1306	GGGAGCTTACTGGAGTTCATAGNAAGTACAGCACATTTTAGGTATGGTTGCCCCGCAAAA	1365
QY	1321	ATTTTGCCCTGCGCAGTTCCTGCTGGAG	1347
Db	1366	TCGAGAGCCGCGCTCTTCTTGTCTCAAG	1392

RESULT 5

```

US-10-424-599-4753
; Sequence 4753, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCES: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 4753
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104297C.1
US-10-424-599-4753

```

Query Match	23.8%	Score 388.8;	DB 12;	Length 1896;
Best Local Similarity	65.4%	Pred. No. 1.2e-105;		
Marthes 570: Conservative	0:	Mismatches 303;	Indels 0;	Gaps 0;

Qy	476	ATAGTGCATCGACATGGGTGGCGACAGACAGACAAAGACACATTATTCAGACGAGATGATTCG 535
Db	623	ATATGTGAATCAGATTCAGATCGGAGAAAGTTGAGATGGAGGATATATTCGAAGAAGACACTG 682
Qy	536	TCATGTGATATTGACAGTGCAGACTCGGGGAAACCCGTTGCTGCAACAGAAATATGTTAAAG 595
Db	683	TTTTGGACATTGATACCTGTGATGCAAAACAACCTCTTGCAGTCGTAGACTATATTGAAG 742
Qy	596	AGCTTTTACACTTTTACAGAGAAANTGAGCTTAAGAGTCTGTGTAAGCCAGATTACATCT 655
Db	743	ATCTTTATGCGCCACTACAGAAAATTGAGGGGTACTAGCTGTCTCTGTGGAATTATGG 802
Qy	656	CCAGCCAAACAGACATAAACTCAAAGATGAGAGCAATCTTGATTGACTGCGCTGATTGAGG 715
Db	803	CACAACAATCTGCACATTAAATGAAAGGATGAGGCTACTACTGATTGACTGCGCTATTGAGG 862
Qy	716	TTCACTACAAGTTTGAACCTGATGGATGAGACGCTCTCTTATGTTAAACATATAAGATA 775
Db	863	TGCACGACAAATTGACCTCTTGACAGAGACATTGTTTCTCACAGTCAATCTTATAGATC 922
Qy	776	GATTCTTTGGAAAAGGAAGTGGTTCCAAAGGAAGACTCAAACTGGTTGGAGTCACAGCTA 835
Db	923	GATTTTGGCAAAAGCACACAGTGGCAAGAAAGCTTCAGTTGGTTGGTCTAGTTGCCA 982
Qy	836	TGCTGCTCGCTGTGTAATATATGAGGAGTATCTGTTCCAGTTGTTGAGGACCTTGTCTGA 895
Db	983	TGCTTTTGGCATGCAAGATGATGAAGAAGTTCTGTACTGTGGTGGGGGATCTAATTCTCA 1042
Qy	896	TATCTGACCGTGCCCTACACAAAAGGGCAAAATTTTAGAAATGGAATAAGTTGATTCTGAACA 955
Db	1043	TATCAGACAAAGCATACACAAGGAAGAAAGTTCTCGAAATGGGAAGTTGATGGTGAACA 1102
Qy	956	CGCTGCAGTTCAAATGCTGTTCCACACCTTATGCTTCATGAACAGAGTTTCTGAAAG 1015
Db	1103	CATTGCAGTTCAAATGCTGTGCGCAACGATACGTTTTTATGAAAAGGTTCTCTAAGG 1162
Qy	1016	CTGCAGATGCAGATAAAACAGCTTCAGCTAGCGTCAATTTTCATGCTCGAAGCTCTGCTGG 1075
Db	1163	CAGCTCAAGCAGACAGAAGCTTCAGTTATGGTTTCTTCTCGTGAAGCTATCTCTTG 1222

RESIT.T 6

US-10-310-154-61

Sequence 61, Application US/10310154
Publication NO. US2003023670A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupalli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deng, Molian
APPLICANT: Dong, Jinzhao
APPLICANT: Duff, Stephen M.
APPLICANT: Galligan, Meghan M.
APPLICANT: Hinchey, Brenda S.
APPLICANT: Huang, Shihshieh
APPLICANT: Johnson, G. Richard
APPLICANT: Jung, Vincent
APPLICANT: Kretzmer, Keith A
APPLICANT: Laccetti, Lucille B.
APPLICANT: Lai, Chao-Qiang
APPLICANT: Lee, Gary
APPLICANT: Lin, Jie-yi
APPLICANT: Liu, Jingdong
APPLICANT: Lu, Bin
APPLICANT: Luethy, Michael M.
APPLICANT: Lund, Adrian
APPLICANT: Madson, Linda L.
APPLICANT: Malloy, Kathleen A.
APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li

TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants

FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 61

LENGTH: 1750
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (114)...(1385)
OTHER INFORMATION:
US-10-310-154-61

Query Match 21.7%; Score 355.4; DB 15; Length 1750;
Best Local Similarity 64.8%; Pred. No. 1.3e-95;
Matches 527; Conservative 0; Mismatches 286; Indels 0; Gaps 0;

```
QY 541 GATATTGACAGTGCAGACTCGGGAAACCGCTTGTGCTGCAACAGATATGTTAAAGAGCTT 600
DB 576 GATATTGACAGTGGTATGACAGAAATTCCTGGCTGGCTGACTATGTAGTAAAT 635
QY 601 TACACCTTTTACAGAGAAATAGGCTAAGAGTTGTGTAAAGCCAGATTACATGTCCAGC 660
DB 636 TACAGATTTTACAGAAACTGAGGGTGCAAGCTCGCTCCCTTACAAATATATGTCAAGC 695
QY 661 CAACAGACATAACTCAAGATGAGAGCAATTCGTATGTAGTGGCTGATGAGGTTAC 720
DB 696 CAACTGATATAAATGAGAAGATGCGTGGCATCTTAATTGACTGGCTCATAGAGGTAC 755
QY 721 TACAAAGTTGAAGTATGATGATGAGAGCTCTTCTTTATGTGTAACATATAGATGATTC 780
DB 756 TACAACTAGAGCTGTGGAGGAGACCTTTTCTTCAACCGTGAACATCATAGACAGATTC 815
QY 781 TTGAAAAGGAAGTGGTCCAGAGGAAGAGCTTAACTGTTGGAGTCACAGCTATGCTG 840
DB 816 TTGGCAGCTGAAATGTGGTGGGAAAGAGCTTCAAGTGTAGTGGTGAAGTCTATGTTG 875
QY 841 CTCGGTGTGAATATGAGGAGTATCTGTTCAGTGTGTGAGGACCTTGTGCTGATATCT 900
DB 876 CTCGGGTGAAGTATGAGAAGTGAAGCTGACCTGTGTGGTGGAGTCTGATCTGATCGT 935
QY 901 GACCGTGCCTACACAAAGGGCAATTTTAGAAATGGAAGTTGATTCGAAACAGCTG 960
DB 936 GATCGTGCATACACAGGGCTGACATCTTGAGATGGAGAGGAGATAGTGAACACACTT 995
QY 961 CAGTTCAACATGTCTGTCCACACCTTATGCTTTCATGAAGAGGTTTCTGAAGCTGCA 1020
DB 996 AATTTCAATATGTGGTGGCTGCTCCATCTGTTTCAATGAGAGGTTTCTAAGGCACGA 1055
QY 1021 GATGCAGATPAAACAGCTTGAAGTACGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAA 1080
DB 1056 CAATCAGAGAAGAGCTGAACTCTCTCTTCTTCAATGATGAGTGGAGTCTTGTGCA 1115
QY 1081 TACCAATGCTGAATATATCGGCTTCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1116 TATGAGATGCTCCAGTCTTGTCCCGCTTATGCTAGCAGCGCTGCCATCTACACCGCTCAA 1175
QY 1141 TGTGCTATCAATCGTTGCCAGCACTGGCAAAAGGCTCTGCGAGTCTCATAGCAGATACACT 1200
DB 1176 TGCACCATAAATGGGTTCAAGTCTTGGAAACAAATGCTGTGAAGTCTGACACAAATATCA 1235
QY 1201 AGGACCAACTCTGAGTGTGCTGAGATGATGGTAGATTTTCAACAGAGGCTGGAACC 1260
DB 1236 GAAGACATCTAATGGTTTGTCTTAGATGATGGTTGAAGTCTGCAACAAAGAGCACTCAT 1295
QY 1261 AGTAAGCTCACTGGCTGCACAGAGGAGTACAGTACCTTCAAGTTCGGTTGGTGGCCCAAG 1320
DB 1296 GGGAAACTTACAGGGTCCATAGAAAGTACACACTTCTAGATATAGCTATGCTGCGAA 1355
QY 1321 ATTTGCTGGCAGGTTCTGCTGGAGTCGGGA 1353
```

DB 1356 TCGGAACCCGCAACTTTCTTGTGGATGCTCGA 1388

RESULT 7

US-10-260-238-497
Sequence 497, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyuki
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 497
LENGTH: 1281
TYPE: DNA
ORGANISM: Oryza sativa
US-10-260-238-497

Query Match 20.9%; Score 342.4; DB 15; Length 1281;
Best Local Similarity 67.8%; Pred. No. 8.7e-92;
Matches 556; Conservative 0; Mismatches 251; Indels 13; Gaps 5;

```
QY 541 GATATTGACAGTGCAGACTCGGGAAACCGCTTGTGCTGCAACAGATATGTTAAAGAGCTT 600
DB 447 GATATTGACAGTGTGATGCAATAACTCCCTTGCAGTAGTTGAAATATGTTGATGAAAT 506
QY 601 TACACCTTTTACAGAGAAATG---AGGCTAAGAGTTGTGTAAAGCCAGATTCATGTCC 657
DB 507 TACAGCTTCTACAGAGGAGTGAAGAGGTTTGAAGCTGTCTCTCTCTAAATACATGTTG 566
QY 658 AGCCAAACACACATAAAGTCAAGAGTGAAGCAATTCGATTGACTGGCTGAT--TGAGG 715
DB 567 AGCCAAATGACATTAATGAGAAGATCGCGGCAATTCATCGATTGGCTGATAGAGG 626
QY 716 TTCACTACAAGTTGAAGTATGATGAGAGCTCTCTCTTCTTATGGTAAACATATAGATA 775
DB 627 TGCATTACAAGTTAGAGCTATTGATGAGAGCTCTCTCTTCTTACTGTGAATATCATAGAC 686
QY 776 GATTTTGGAAAGGAGTGGTTCCAAAGGAAGAGCTCAACCTGGTTGGAGTCACAGCTA 835
DB 687 GATTTTGGCTCCGAAATGTTGGTGGAAAGAGCTTCAGTTGGTTGGCTGACTGCCA 746
QY 836 TGCTGCTCGCTTGTAAATATGAGAGGATATCTGTTCCAGTTGTGAGGACCTTGTGCTGA 895
DB 747 TGCTGCTCGCTGCAAGTATGAAGAGTGAAGCTTCTCTGTAGTGAAGGATCTTATCTTAA 806
QY 896 TAICTGACCTGCTTACACAAAGGGCAATTTTGAAT--GAAAAGTTGATTTCTCAAC 954
DB 807 TCTGCGACCGCTTACACAAAGAGATATCTCGAAATGGAGAGGATGATTTGTAAC 866
QY 955 ACGCTGAGTTCAACATGTCTGTTCCAAACACCTTATGTCTTCAATGAAGAGGTTCTGAAA 1014
DB 867 ACTCTTCAGTTGATGATGTCAGTTCCAACTCCATACTGTTTCAATGAGAAGTTCTCCTCAAG 956
```

QY 1015 GCTGCGATGACAGAT-----AAACAGCTTGTAGCTAGCTGCTATTTTTCATGCTGAGCTC 1068
Db 927 GCTGCGAATCTGACAGAAAGAACAGCTTGTAGCTGCTATTTTTCATGCTGAGCTG 986
QY 1069 TGTGTTGTAAGAACCAATGCTGAATTTATGCGCTTGGCATCTGCTGCTGCTGCTGCTG 1128
Db 987 AGCTTGTGAGTATGAGATGCTCAATTTCCAGCTTCAATGCTGCGGCTGCTGCTGCTG 1046
QY 1129 TATCTGACAGTGTGCTATCAATGCTTGGCAGCATGGAACAAAGCTTGGAGTCTCAT 1188
Db 1047 TACATGCTGCTGAGTGCACCATTAATGCTTCAAGTCTTGGAAACAAATGCTGCTGAGTGCAT 1106
QY 1189 AGCAGATACACTAGCGACCACTCCT--GGAGTCTGAGATGATGCTAGATTTTCAACA 1247
Db 1107 ACATATCTCTGAGAGACAGCTGATGAGAGTCTCAAGATGATGCTGAGCTCCACCA 1166
QY 1248 GAAGGCTGGAACCAAGTAACTGCTGCTGCGAGAGTACAGTACCTCAAGTTCGG 1307
Db 1167 AAAAGCAGGACATGGGAAGCTTACTGAGTTTATAGAAAGTACAGCACATTTAGSTATGG 1226
QY 1308 TTGCGTGGCCAGATTTTGGCTGCGCAGTTTCTGCTGCTGGAG 1347
Db 1227 TTGCGCCGCAAAATCGAGGCCCGCTTCTTCTGCTCAAG 1266

RESULT 8

US-10-310-154-51
Sequence 51, Application US/10310154
Publication No. US20030233670A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H.
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupallli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deng, Molian
APPLICANT: Dong, Jinchuo
APPLICANT: Duff, Stephen M.
APPLICANT: Galligan, Meghan M.
APPLICANT: Hinchey, Brenda S.
APPLICANT: Huang, Shihshieh
APPLICANT: Johnson, G. Richard
APPLICANT: Jung, Vincent
APPLICANT: Kretzmer, Keith A.
APPLICANT: Lacchetti, Lucille B.
APPLICANT: Lee, Gary
APPLICANT: Lin, Jie-Yi
APPLICANT: Liu, Jingdong
APPLICANT: Lu, Bin
APPLICANT: Luerhy, Michael M.
APPLICANT: Lund, Adrian
APPLICANT: Madson, Linda L.
APPLICANT: Malloy, Kathleen A.
APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang

APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 51
LENGTH: 1751
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (82)...(1518)
OTHER INFORMATION:
US-10-310-154-51

Query Match 14.9%; Score 243.8; DB 15; Length 1751;
Best Local Similarity 56.0%; Pred. No. 5.5e-62;
Matches 461; Conservative 0; Mismatches 362; Indels 0; Gaps 0;
QY 541 GATATTGACAGTGCAGACTCGGGAAACCCGCTTGTCTCAACAGATATGTTAAAGAGCTT 600
Db 709 GACATTGATGCACCTGATTTCTTCAATGAGCTGCGTGTGAATATGTTGAGGACATT 768
QY 601 TACACCTTTTACAGAGAAATGAGGCTTAAGAGTTGTGTAAGGGCCAGATTTACATGTCAGC 660
Db 769 TACAGATTCTACAGAGACACTGAGGGCACCTGCTTCTCTCAGCAGCTACATGAGCTCA 828
QY 661 CAACAAGACATAAATCAAGATGAGAGCAATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 829 CAGGCTGAATCAGTGAAGAGATGAGAGCTATCCTTATGCTGCTGCTGCTGCTGCTGCTGCTG 888
QY 721 TACAAGTTTGAATGATGATGAGAGCTGCTTCTTCTTATGTTAAACATAATAGATGATTC 780
Db 889 TACAGGCTTACTCTAATGCCAGAGACACTTTACTTTCGCTGCTACATCATGACCACTAC 948
QY 781 TTGGAAGAGAGTGTGTTCCAGAGAGAGTACAACTGTTGAGTGCAGAGTACAGCTATGCTG 840
Db 949 TTATCTATGAGAGTGTACCAAGAGAGAGCTACAGCTGCTGCGGCAATGAGTGCCTATGCTG 1008
QY 841 CTCGCTTCTAAATATGAGGAGTATCTGTTCCAGTGTGTTGAGGACCTTGTCTGCTGATATCT 900
Db 1009 ATAGCAAGCAAGTACGAGAGATATGGCTCCACTGTTTAAAGACTTGTATGCTGCTATGT 1068
QY 901 GACCGTGCTACACAAAAGGGCAATTTTGAATGAGAAAGTTGATTTGAAACACGCTG 960
Db 1069 GACAACGCAATTTACCAGAGAGACCAATTTGACCAAGGAGGAGGCAATCTGAGCATGCTC 1128
QY 961 CAGTTTCAACATGCTGTTTCCAAACACCTTATGTTCTTGAAGAGAGTTTCTGAAAGCTGCA 1020
Db 1129 CATGGAACTGACGGTTTCCAAACATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1188
QY 1021 GATGAGATAAACAAGCTTGTAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1189 ATGTGTGAGCAGAGCTTGAAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATG 1248
QY 1081 TACCAAAATGCTGAATTTATGCGCTTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1249 TACGGATGCTGTTTATCTTCCATCGGTGACCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTG 1308
QY 1141 TGTGCTATCAATCGTTTGGCAGCAGTGGCAAGAGTCTCGAGTCTCATAGAGATGATACACT 1200
Db 1309 TCTACACTTGGGATGAATCCACAGTGGAGTATTTCTGGAACATCATCACTGGGCTAGCT 1368
QY 1201 AGCGACCAACTCTCGAGTGTCTGAGGATGATGTTTCTGAGGAGGCTGGAAC 1260
Db 1369 GAGCCACAGTTTACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1428
QY 1261 AGTAAAGTCACTGGGCTGCACAGGAGTACAGTACCTACAAGTTGCTGCTGCTGCTGCTGCT 1320

Db 1429 AGCAAGCAAAAGGCGGTGTACAGGAAGTACTCCAAGCCAAAGCTCGGCTCGTGCCTG 1488
QY 1321 ATTTTGGCTGGCGAGTCTCTGCTGGAGTCGGAGGACACCGC 1363
Db 1489 CAATCCCTGACAAAGAGCTGTGTGACAGTTGAGGCTCGCTGC 1531

RESULT 9
US-10-424-599-118853
; Sequence 118853, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 118853
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1141)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; .OTHER INFORMATION: Clone ID: PAT_MRT3847_78333C.1
US-10-424-599-118853

Query Match 14.0%; Score 228.6; DB 12; Length 1141;
Best Local Similarity 56.7%; Pred. No. 1.5e-57;
Matches 442; Conservative 0; Mismatches 334; Indels 3; Gaps 1;

QY 568 CGCTTGTGTGCAACAGATATGTTAAAGAGCTTTTACACCTTTTACAGAGAAATGAGCT 627
Db 30 CGCTTGTGTGTGGAGTCAATGATGACATTTTACAAAGTTTCTACAACTTTGTTGAAAC 89
QY 628 AAGAGTTGTGTAAAGCCAGATTACATGTCACGCAACAAAGACATAAACTCAAGATGAGA 687
Db 90 GAGA---GCCACCCACGACTACATTGATTCACACCTGAATTAATGAGAGATGAGA 146
QY 688 GCAATCTGATGACTGGCTGATGAGGTTCACTACAAAGTTTGAAGTGAATGATGAGAGC 747
Db 147 GCTATCTGTTGATGTTGGCTGATAGACGTTTACACCAAGTTTGAACCTTCTCTAGAGACC 206
QY 748 CTCCTTCTATGTTAAACATAATAGATAGATTCTTGGAAAAGGAAGTGGTTCCCAAGGAAG 807
Db 207 CTTTACCTGACCATCAACATATTTGATCGGTTTGTAGCAGTTAAGACAGTTCCAAGGAGG 266
QY 808 AAGCTAACACTGGTTGGAGTCACAGCTATGCTGCTGCTTGTAAATATGAGAGGATATCT 867
Db 267 GAACCTGCAATTTGGTTGGCATCAGTGCCTGCTGATGAGTCCCAATATGAGAAATCTGG 326
QY 868 GTTCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACAAAGGSCAAAT 927
Db 327 CCCCTGAGTTAATGATTTGTGTGCTCTCAGATAGGGGTTTACCTCATGAACAGATA 386
QY 928 TTAGAAATGGAAGTTGATTTCTGAACACGCTGAGTTTCAACATGCTGTGTTCCAAACCT 987
Db 387 CTGGCCATGGAGAAAACCATATTAATTAAGCTGAATGGACTTTGACCTGCTGCCTACACCT 446
QY 988 TATGCTTTCATCAAGAGCTTTCTGAAAGCTGCAGATGAGATAAACAGCTTGACCTAGCG 1047
Db 447 TTGTTTTCCTAGTTGCTTTTATCAAGGACGCGTCCAGATCAGGAGTTGGAAGAACATG 506
QY 1048 TCATTTTTCATGCTGGAGCTGCTGTTGGTAGAATACCAAAATGCTGAATTTATCGGCTCTG 1107
Db 507 GCTCATTTTATGCTGAGTTGGGAATGATGAATGACATGCAACCTTAATGATGCTGCCATCA 566

QY 1108 CATCTGGCTGCTGCTGGGTTTTACTGCACAGTGTGCTATCAATGTTGCCAGACTGG 1167
Db 567 ATGTTGCTGCTCTCAGCAGTGTTCAGCAAGATGCACTCTGAACAAGCTCCCTTTGG 626
QY 1168 ACAAGGCTCTGAGTCTCATAGCAGATACACTAGCAGCAACTCTCTGGAGTGTGAGG 1227
Db 627 AATGAGACACTTAAGCTGCACACTGGTTACTCAAGAGCAACTCATGGATTGTGCTAGA 686
QY 1228 ATGATGTTAGATTTTCCACCAGAGGCTGGAACCACTAGCTCAGTGGGTCACAGGAG 1287
Db 687 CTATTGGTGGGTTCCATTCCCACTTTGGGAATGAAAGCTTAGGGTTGTGTACAGAAAG 746
QY 1288 TACAGTACCTACAAGTTGCTGCGTGGCCAAAGATTTTGCCTGSCGAGTTCCTGTGGA 1346
Db 747 TACTCTGACCTCAGAAGGGTGCAGTTGTGTGCTGCCACCTGCTAAACTTCTGCTGA 805

RESULT 10
US-10-260-238-1251
; Sequence 1251, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Rumiya
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rickes, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1251
; LENGTH: 1384
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: (610)..(610)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (668)..(668)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (676)..(676)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (898)..(898)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-1251

Query Match 14.0%; Score 228.6; DB 15; Length 1384;
Best Local Similarity 56.4%; Pred. No. 1.8e-57;
Matches 482; Conservative 0; Mismatches 368; Indels 5; Gaps 3;

QY 524 AAGATCAATGCTCATGGATATTGACGTGCAAGCTCGGGAAACCCGTTGCTGCAACAG 583

Db 391 AAAAGGAGCTGATATACGACATCGATGCTATCTGCTCACAAAGAGCTGGCAGTGATTG 450
QY 584 AATATCTTAAAGAGCTTACACCTTTTACAGAGAAAATGAGGCTAAGAGTTGTGTAAGGC 643
Db 451 ATTACGTCGAAGATATCTACAGATTCTACAGAGCACTGAGAGAACACCTACCGGCTCT 510
QY 644 CAG--ATTACATGCTCAGGCAACAGACATAAATCAAGATGAGAGCAATTTCTGATGA 701
Db 511 CTGCACTCATGCTGTCAGACCGAGATCAACGAGAAATGAGAGCAATCTCTACGTA 570
QY 702 CTGCTGATGAGGTTCACTACAAAGTTTGAATGATGAGAGCTCTTTCTTATGGT 761
Db 571 TTGGCTCATCGAAGTCACTACAGGCTTATGCTGATGCCGAGACCTTGCTACCTCT 630
QY 762 AATCATATAGATAGATTCTTGAAAGAAAGAGTGGTTTCAAGAGAGAGCTACAAGTGT 821
Db 631 CTACATAATGATCAGTACCTGTCCTGAGAAATGTCGAGAAAGAGCTGAGCTTGT 690
QY 822 TGAGTCAACAGCTATGCTGCTGCTGTTGTAATATGAGAGGATCTGTTCCAGTTGTTGA 881
Db 691 CGAGTAAGGCCATGTTGATAGCTGCGAATGAGAGACTTGGGCTCCA-TTGTAA 749
QY 882 GGAACCTTGTGCTGATATCGACCGTGCCTACACAAAGGGCAAAATTTAGAAATGGA 941
Db 750 GGAACCTTGTGCTGATATCGACAACTCTTACAGAGGAGAGGTTCTGAGCAGAGAA 809
QY 942 GTTGATTTCAACAGCTGAGTTCAACATGCTGTTCCAAACACCTTATGTTCTCATGAA 1001
Db 810 GTCCATATTAACAGCTCAGTGGAACTGATGTTCCGACATGCTACATGTTCTAT 869
QY 1002 GAGTTTCTGAAAGCTGAGATGAGATAA--ACAGTTGAGTAGCGTCAATTTTCATG 1059
Db 870 TCGATACCTGAAAGCTGATGCTGCTGACNAGAGAGCTGAGCACAATGACTTCTTCTAC 929
QY 1060 CTGAGCTGCTGCTGTTAGATACCAATGCTGAATTCGCTTCCGCTTCGCTGCT 1119
Db 930 GCAAGCTCGACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989
QY 1120 GCTGCGGTTTATCTGACAGTGTGCTATCAATCGTTGCGAGCACTGGAACAAGGCTG 1179
Db 990 GCTGCGCTCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049
QY 1180 GAGTCTCATAGATACACTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1239
Db 1050 GAGTACCAACCGGCTTAGCTGAGCGCAATGCTGAGTGTGCGAGGCGCTGCTGAGC 1109
QY 1240 TTTACAGAGGCTGGAACAGTAACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1299
Db 1110 CTGCAAGCGGCGGCGGAGAGCAGCAGAGTGTGTACAAAGTACGCGAGCGCC 1169
QY 1300 AGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1359
Db 1170 AAGCTCGGAGCGGCT 1229
QY 1360 CCGCT 1374
Db 1230 GTGGCGGCTTGAGCT 1244

RESULT 11

US-10-424-599-103481
; Sequence 103481, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 103481
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64461C.1
US-10-424-599-103481

Query Match

13.5%; Score 220.6; DB 12; Length 1944;
Best Local Similarity 56.9%; Pred. No. 5.8e-55;
Matches 466; Conservative 0; Mismatches 344; Indels 9; Gaps 3;

QY 529 GAATGCTCATGATATTGACAGTGGAGACTCGGGAAACCCGCTTGCTGCTCAACAGAAATAT 588
Db 856 GAGTTTGTGATGACATTGATGCACTGACATGACAAATGAAATGGCAGCCGAGTAC 915
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAGCCAGAT 648
Db 916 ATCGATGATATCTACAAATTTTACAAAGAGACTGAAAGAGATGGTTGTGT--GCAATGAC 972
QY 649 TACATGCCAGCCAAAGACATAAACTCAAAGATGAGAGCAATTTCTGATTTGACTGGCTG 708
Db 973 TACATGGTTGCGAGCCAGATATTAATGCCAAGTGAAGTCAATCTTTGTTGGACTGGTTG 1032
QY 709 ATTGAGTTCACTACAAAGTTTGAATGATGATGAGAGCGCTCTTTCTTATGTTAAACATA 768
Db 1033 ATAGAAGTCAATAGGAAGTTTGAAGCTCATGCCAGAACTCTTTATTTGACCTTGAACATT 1092
QY 769 ATACATAGATTCTTGGAAAGGAGTGGTTCCAAAGGAAGAGCTACAACTGGTTGGAGTC 828
Db 1093 GTGATCGTTTCTGCTGTAAGGCTGCTGCTGTAAGGAGCTTCAAGGAGCTTCACTGTTGGCATC 1152
QY 829 ACAGTATGCTGCTGCTGTTGTAATATGAGAGGATCTGTTTCAGTTGTTGAGGACCTT 889
Db 1153 AGCTCAATGCTGATGAGCTCATAAATATGAAGAGATATGGCACACAGAGTTAATGACTTT 1212
QY 889 GTGCTGATATCTGACCGTGGCTACACAAAGGGCAAAATTTAGAAATGGAAGTTGATT 948
Db 1213 GTGTGCTATCAGACAAATGCTTATGTTAGTGAACAGTGTGATGATGAGAGAAACAATC 1272
QY 949 CTGAACAGCTGCTGAGTTCAACATGCTGTTCCAAACACCTTATGTTCTTCATGAAGAGTTT 1008
Db 1273 CTAGGAAGCTTGAATGCTACTTAAACAGTTCCAAACACCTTATCACTTCTTGGTTAGGTAT 1332
QY 1009 CTGAAGCTGAGAT--GCAGATAACAGCTTGAAGTGGCTAGGCTCATTTTTCATGCTGAG 1065
Db 1333 ACCAAAGCTTCCACTCCGCTGCAAAAGAGATGGAACATGTTGTTTTCCTTCTGCTGAA 1392
QY 1056 CTCTGCTTGTAGAAATACCAAA--TGCTGAATATCGGCTTTCGCAATCTGGCTGCTGCT 1122
Db 1393 CTGGAATGATGCTTATCTCTACTGTAATCTTTGACGCTCTTCTCTGATGCTGCTTCT 1452
QY 1123 GCGTTTATCTGACAGTGTGCTATCAATGTTGCCAGCACTGGAACAAGGTTCTGCGAG 1182
Db 1453 GCTGTGTTGCGGCTCGATGTACCTTTGGAAGGAGCCCTTTCTTGGACAAACACTTTGATG 1512
QY 1183 TCTCATAGCATACACTAGCGACCAACTCTCTGAGTGTCTCGAGATGATGTTAGATTTT 1242
Db 1513 CACTACACAGGCTACTCTGAGGACCACTAAGGATTTGGGCCAAATCATGGCCAACTT 1572
QY 1243 CACCAAGAGGCTGGAACAAGTAAAGTCACTGCTGCTGACAGGAGTACAGTACCTACAG 1302
Db 1573 CATGCTGCTGCAACAGGAAAGTAAAGCTTAGGCGAGTTTACAGAAATTTCTTAACTCGAT 1632
QY 1303 TFCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1341
Db 1633 CTTTCTGCTGTTGCTTCTTCTTCTCCAGCAAGGACTTG 1671

RESULT 12

US-10-424-599-118855
; Sequence 118855, Application US/10424599

Db 951 CCTGTCCGCTTCATCAAGCTTCGATGTCATCCAGAAATGGAGATATGTTCACTT 1010
Qy 1056 CATGCTGGAGCTCTGCTGGTAGATACCAAAATGCTGAATATCGGCTTCGCATCTGGC 1115
Db 1011 CCTGTGTAATGGGGATGATGATACGACACCTTGACGTTCTGTCCCTCCATGCTTGC 1070
Qy 1116 TGTGCTGCGGTTTATCTACTGACAGTGTCTATCAATCGTTGCCAGCATGGACAAAGT 1175
Db 1071 TGTCTCAGCTGTTACACGGCAGATGCTCATTTGAACAAGTCCCTGCTTGACTGATAC 1130
Qy 1176 CTCGAGTCTCATAGCAGATACACTAGCAGCACTCTGGAGTCTGGAGTCTGGAGATGATGT 1235
Db 1131 ATTGCAAGTTCCACACCGGCTACACAGAGTCTGAGATTTAGACTGCTCAAGCTTTTAGC 1190
Qy 1236 AGATTTTCCACCAAGGCTGGAACCACTGAGTCTGCTGCTGCAAGCAAGTACAGTAC 1295
Db 1191 TTTTCTTCACTCAGATGCGGTGAGAGCAGGCTACGTGCAGTCTCAAGAAGTACTCGAA 1250
Qy 1296 CTACAAGTTCCGTTGGTCCCAAGATTTTGGCTGCGCAATTCCTGCTG 1344
Db 1251 GGCAGAGATGGAGGTGTTGCTATGTTTCTCCGGCCAAAGTCTCTCTTG 1299

RESULT 14

US-09-938-842A-789

; Sequence 789, Application US/09938842A

; Publication No. US20040009476A9

; GENERAL INFORMATION:

* APPLICANT: Harper, Jeff

* APPLICANT: Krepis, Joel

* APPLICANT: Wang, Xun

* APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 789

; LENGTH: 1338

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-789

Query Match 13.1%; Score 214.6; DB 11; Length 1338;
Best Local Similarity 54.5%; Pred. No. 2.8e-53;
Matches 452; Conservative 0; Mismatches 374; Indels 3; Gaps 1;
Qy 516 TATGACGAAGATGAATGCTCATGGATATGACAGTGCAGCTCGGGGACCGCTTGC 575
Db 474 TATAGTCAACAAACCAAGATTTATCGATTTATGATGATCTGACAAAGATAACCATTTGGC 533
Qy 576 TGCAACGAATATGTTAAGAGCTTTACACCTTTTACAGAGAAATCAGGCTAAGAGTTG 635
Db 534 TCGGCTGAGATGTTGATGATGATGATCTCGTTCTTATAAGAAGTTGAGAAGGAGACTCA 593
Qy 636 TGTAGGCCAGATTTACATGTCACGCAACAGACATAAACTCAAGATGAGAGCAATCT 695
Db 594 GCCTAAGATG---TACATGCACTTCAGACTGAAATGAATGAGAAGATGAGAGCGATCTT 650
Qy 696 GATTGACTGGCTGATTGAGGTTCACTACAAGTTTGAAGTATGATGATGAGAGCGCTTTCT 755
Db 651 GATTGATTGGTTACTAGAGTTTACATCAAGTTTGGAGCTCAACCTTGAACCTCTGTACCT 710
Qy 756 TATGTTAAACATAATAGATAGATTTCTGGAAAAAGAGTGGTTCCAGAGGAAGAGTACA 815
Db 711 CACCCTCAACATCATTTGATGATGATCTCTCTGTGAAAGCTGTCCCTAAAGAGAGTTACA 770

APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vicaya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanquo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 52
LENGTH: 1850
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (254)..(1579)
OTHER INFORMATION:
US-10-310-154-52

Search completed: March 20, 2004, 23:16:41
Job time : 590 secs

Query Match 13.0%; Score 212.8; DB 15; Length 1850;
Best Local Similarity 56.6%; Pred. No. 1.2e-52;
Matches 466; Conservative 0; Mismatches 337; Indels 21; Gaps 3;
Qy . 530 AATTGCTCAGGATTTGACAGTGCAGACTCGGGGAAACCCGCTTGTGTCACACAGATATG 589
Db 747 AAGTGGTCGATGACATCGCAAGCTGACGCTCAACATGAGCTCGCGGTGGTGAATACA 806
Qy 590 TTAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAGGCCAGATT 649
Db 807 TTGAGGACATCTACAGTTCTACAGATTGCTCAGCAGAGACGCCCATG---TGACT 863
Qy 650 ACATGTCAGCCACACAGACATAACTCAAAGATGAGAGCAATCTGATTGACTGCTGA 709
Db 864 ACATCGACGCCCACTCGAGATCAACTCTAAGATGAGGGCTATCCTGGCTGATTGGATAA 923
Qy 710 TTGAGGTTCACTACAAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 769
Db 924 TTGAAGTACACCAAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 983
Qy 770 TAGATAGATTCTTGGAAAAGGAAGTGTTCACAGAAAGAGTACACTGTTGGAGTCA 829
Db 984 TCGATCAGTACCTCTCGCTGCAACACAGTCTCGTGAAGGAGTGCAGCTTGTTCGGGTTT 1043
Qy 830 CAGCTATGCTGCTCGCTGTAAATATGAGAGGATATCTGTTCCAGTTGTTGAGGACCTTG 889
Db 1044 CATCTATGCTGATCGCTGCAAGTACGAGGAGATTTCGGGCCCGAGGTTGAACGACTCA 1103
Qy 890 TGCTGATATCTGACCGTCTTACACAAAAGGGCAAAATTTAGAAATGAAAAGTTGATTC 949
Db 1104 TCCTCATATCAGACAGTGCATACAGTAGAGAACAGATTCTTTCGATGGAGAGGGATTC 1163
Qy 950 TGAACAGCTCAGTTCAACATGCTGTTCACACACCTTATGCTTTCATGAAGAGGTTTC 1009
Db 1164 TGAATAGGCTGGAGTGAACCTGACTGTCCCTACAGTGTATGTTCCCTTGTCCGTTTTC 1223
Qy 1010 TGAAGCTGTCAG-----ATGCAGATAAACAGCTTGAGCTAGCGTCAATTTTCA 1057
Db 1224 TGAAGGCGCGAACATTGGCGCGCAAGTTGAGAAAGAGATGGAATATGGTGTCTTCT 1283
Qy 1058 TGCTGAGCTCTGCTGTGTGATAGATACCAATGCTGAATATTTCGGCCCTTCGATCTGGCTG 1117

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 20, 2004, 19:33:10 ; Search time 4447 Seconds
(without alignments)
10985.952 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1636
Sequence: 1 tcacggggctctccgtccg.....aaaaaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum Match 100%
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: go_estl.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estcom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_nam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gasl.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1534	99.9	1655	11	AY104859
2	598.8	36.6	863	14	CA280467
3	597.2	36.5	613	14	CD001829
C 4	596	36.4	607	10	AW256237

C	5	585.8	35.8	589	12	BG268357
	6	579	35.4	579	14	CD001830
	7	570.2	34.9	574	14	CA249171
	8	552	33.7	563	13	CA122466
	9	531.6	32.5	586	9	AI770352
C	10	512.6	31.3	742	13	CA122563
C	11	502.4	30.7	683	14	CA223571
C	12	485.2	29.7	778	29	CG453107
C	13	485.2	29.7	779	29	CG453099
C	14	485.2	29.7	873	29	CG278953
	15	482	29.5	626	13	CA101841
	16	471.4	28.8	625	13	CA085373
	17	469.2	28.7	646	14	CA223491
	18	463	28.3	463	10	B8638542
C	19	462.8	28.3	553	14	CF036794
C	20	452	27.6	717	14	CA299622
	21	450	27.5	631	13	CA083532
C	22	443.4	27.1	690	14	CF625999
	23	430.4	26.5	577	14	CA292585
	24	429.6	26.3	623	14	CB882198
C	26	423.4	25.9	956	29	CG214272
C	27	420.2	25.7	868	29	CG293488
	28	418.4	25.6	982	10	B8040145
	29	411.2	25.1	580	14	CA269779
	30	410	25.1	944	29	CG293502
	31	402	24.6	525	12	B1099542
	32	390	23.8	608	14	CA831492
C	33	387.6	23.7	564	14	CA292710
	34	386.4	23.6	817	10	B2481509
	35	384.4	23.5	817	14	CB000327
	36	358.6	21.9	1643	11	AV111119
	37	357.4	21.8	500	14	CF772280
	38	339.8	20.8	490	12	B1411133
	39	328.6	20.1	686	14	CA253051
C	40	326.2	19.9	356	9	AI629483
C	41	326.2	19.9	400	13	BQ538226
	42	320	19.6	507	13	BU101379
	43	314.6	19.2	615	14	CA242395
	44	309	18.9	666	13	CA074749
	45	307.6	18.8	596	14	CA999572

ALIGNMENTS

RESULT 1
AY104859
LOCUS Zea mays PC0144752 mRNA sequence.
DEFINITION Zea mays PC0144752 mRNA sequence.
ACCESSION AY104859
VERSION AY104859.1 GI:21207937
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1655)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
AUTHORS Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1655)
Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

linear HTC 16-OCT-2002

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

source

Location/Qualifiers

1..1655
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match	99.9%;	Score 1634;	DB 11;	Length 1655;
Best Local Similarity	99.9%;	Pred. No. 2.1e-235;		
Matches 1634;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 TCACGGGGCTCCCTCCGTCCTAGGACACCGCCACGCTCTCGGCTGGATCAACAGGCGG 60

DB 20 TCACGGGGCTCCCTCCGTCCTAGGACACCGCCACGCTCTCGGCTGGATCAACAGGCGG 79

QY 61 GCCGATCCGCTCTTCCCTCTCTCTCGGGTCCGGCTTGGGGATCATGGCGGCGGG 120

DB 80 GCCGATCCGCTCTTCCCTCTCTCTCGGGTCCGGCTTGGGGATCATGGCGGCGGG 139

QY 121 GCCGCTGACGAGAACAGGAGACCGCGGGCGAGGAAGCCCGCCAGGCTCCGAGACATG 180

DB 140 GCCGCTGACGAGAACAGGAGACCGCGGGCGAGGAAGCCCGCCAGGCTCCGAGACATG 199

QY 181 GCCGAGCGGCGCGCTCAGGACATCAAGAACTCTGTCGGGCTCCCGCTACCCCTAC 240

DB 200 GCGAGCGGCGCGGCTCAGGACATCAAGAACTCTGTCGGGCTCCCGCTACCCCTAC 259

QY 241 GCCGTCGCCAAGAGCCCATCTGTCAGAGAGCAAAAGGAGCAAAAGCAGCCAGGCTTG 300

DB 260 GCCGTCGCCAAGAGCCCATCTGTCAGAGAGCAAAAGGAGCAAAAGCAGCCAGGCTTG 319

QY 301 GCAGAGCGGCGGCGCTCAGGAAATTCGCGCTCTCTGCGAGAGGCGGCGCAACCT 360

DB 320 GCAAGCGGCGGCGGCTCAGGAAATTCGCGCTCTCTGCGAGAGGCGGCGCAACCT 379

QY 361 GAATGTCAGCGGCTGATGATCCAGAACCCGAGCTTTGTCAACAGAGGAATCAGTA 420

DB 380 GAATGTCAGCGGCTGATGATCCAGAACCCGAGCTTTGTCAACAGAGGAATCAGTA 439

QY 421 GCGATGCGCAGCTGATGATGAGTGAATCTACGAGCTGTCGAGCGGTAGTATGAT 480

DB 440 GCGATGCGCAGCTGATGATGAGTGAATCTACGAGCTGTCGAGCGGTAGTATGAT 499

QY 481 GACATCGACATGGGTGCGACAGAGAACAGGACATTTATGACGAAGATGAATGCTCATG 540

DB 500 GACATCGACATGGGTGCGACAGAGAACAGGACATTTATGACGAAGATGAATGCTCATG 559

QY 541 GATATTGACATGAGCTCGGGNAACCGGCTTCTGTCACAGATATGTTAAAGACTT 600

DB 560 GATATTGACATGAGCTCGGGNAACCGGCTTCTGTCACAGATATGTTAAAGACTT 619

QY 601 TACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAAGCCAGATTACATGCCAGC 660

DB 620 TACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAAGCCAGATTACATGCCAGC 679

QY 661 CAACAGACATAAATCAAGATGAGAGCAATTCGATTTGACTGGCTGATTTGAGGTTTAC 720

DB 680 CAACAGACATAAATCAAGATGAGAGCAATTCGATTTGACTGGCTGATTTGAGGTTTAC 739

QY 721 TACAAGTTTGAATCATGATGAGAGCTCTTCTTATGTTAAACATAATAGATGATTC 780

DB	740	TACAAGTTTGAATCATGATGAGAGCTCTTCTTATGTTAAACATAATAGATGATTC	799
QY	781	TTGGAAAAGAACTGCTTCCAGGAGAAAGCTACAACTGTTGGAGTCAAGCTATGCTG	840
DB	800	TTGGAAAAGAAAGTGGTTCAGAGAAAGAACTACAACTGTTGGAGTCAAGCTATGCTG	859
QY	841	CTGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCT	900
DB	860	CTGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCT	919
QY	901	GACGTCCTTACACAAAAGGCAAAATTTAGAAATGAAAAGTTGATTTCTGAACACGCTG	960
DB	920	GACGTCCTTACACAAAAGGCAAAATTTAGAAATGAAAAGTTGATTTCTGAACACGCTG	979
QY	961	CAGTTCAACATGCTCTTCCAAACACCTTATGCTTTCATGAAGAGGTTTCTGAAGCTGCA	1020
DB	980	CAGTTCAACATGCTCTTCCAAACACCTTATGCTTTCATGAAGAGGTTTCTGAAGCTGCA	1039
QY	1021	GATCAGATAAACAGCTTGAAGCTAGGCTGATTTTTCATGCTGAGCTCTGCTGGTAGAA	1080
DB	1040	GATCAGATAAACAGCTTGAAGCTAGGCTGATTTTTCATGCTGAGCTCTGCTGGTAGAA	1099
QY	1081	TACCAATGCTGAATTTATCGGCTTTCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTG	1140
DB	1100	TACCAATGCTGAATTTATCGGCTTTCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTG	1159
QY	1141	TGCTCTATCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200
DB	1160	TGCTCTATCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1219
QY	1201	AGCGACCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1260
DB	1220	AGCGACCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1279
QY	1261	AGTAAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1320
DB	1280	AGTAAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1339
QY	1321	ATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380
DB	1340	ATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1399
QY	1381	TAGTTGAATCGACCTATTCAACTGGTGGATTTTTTAAAGTTTAAAGTATCTCCATGAA	1440
DB	1400	TAGTTGAATCGACCTATTCAACTGGTGGATTTTTTAAAGTTTAAAGTATCTCCATGAA	1459
QY	1441	CAAGATGAGAAACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1500
DB	1460	CAAGATGAGAAACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1519
QY	1501	TTATGATTAAACAACTTTTTTTTATCTATGTTGAATGACGAGTCAAGTCAAGTCAAGT	1560
DB	1520	TTATGATTAAACAACTTTTTTTTATCTATGTTGAATGACGAGTCAAGTCAAGTCAAGT	1579
QY	1561	TGCTTGTGCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1620
DB	1580	TGCTTGTGCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1639
QY	1621	AAAAAAAAAAAAAAAAAAAA 1636	
DB	1640	AAAAAAAAAAAAAAAAAAAA 1655	

RESULT 2

CA280467	863 bp	mRNA	linear	EST 26-SEP-2003
LOCUS	SCVPFLIC09F11.9	Fl1 Saccharum officinarum	cDNA clone	SCVPFLIC09F11
DEFINITION	5', mRNA sequence.			
ACCESSION	CA280467			
VERSION	CA280467.1	GI:36008161		
KEYWORDS	EST.			
SOURCE	Saccharum officinarum			
ORGANISM	Saccharum officinarum			

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: C09 row: F column: 11

Seq primer: T7 Promoter Primer.

FEATURES

source

1..863

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCVPFL1C09F11"

/lab_host="DH10B"

/clone_lib="FL1"

/note="Organ: Inflorescence at beginning of development

(1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;

An unidirectional cDNA library generated from

inflorescence at beginning of development (1cm-long)].

cDNA was prepared from polyA+ mRNA using SuperScript

plasmid system kit (Invitrogen). The double-strand cDNAs

were fractionated in a sepharose CL-2B 40cm-columns and

fragments sizing between 0.8 and 1.5 Kb were

directionally cloned into the vector. Details of each

source of RNA and library construction can be obtained at

http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 36.6%; Score 598.8; DB 14; Length 863;
Best Local Similarity 92.2%; Pred No. 2.9e-80;
Matches 642; Conservative 0; Mismatches 52; Indels 2; Gaps 1;

QY 881 AGGACCTTGTGCTGATATCTGACCGTGCTACAAAAGGCAAAATTTAGAAATGAAA 940
DB 1 AGGACCTTGTGCTGATATCTGACCGTGCTACAAAAGGCAAAATTTAGAAATGAAA 60

QY 941 AGTTGATTCGAACAGCTGCAGTCAACATGCTGTTCACACCTTATGCTTCATGA 1000
DB 61 AGTTGATTCGAACAGCTGCAGTCAACATGCTGTTCACACCTTATGCTTCATGA 120

QY 1001 AGAGGTTTCTGAAGCTGCAGATGCAGATAAACAGCTTGAGCTAGCGTCATTTTCATGC 1060
DB 121 AGAGGTTTCTGAAGCTGCAGATGCAGATAAACAGCTTGAGCTAGCGTCATTTTCATGC 180

QY 1061 TGGAGCTCTGCTGTGATACCAAGCTGATTAATTCGGCTTCGATCTGCTGCTG 1120
DB 181 TGGAGCTCTGCTGTGATACCAAGCTGATTAATTCGGCTTCGATCTGCTGCTG 240

QY 1121 CTGCGGTTTATCTCCAGTGTGCTATCAATCGTTGCCAGCACTGGACAAAGGTCCTGCG 1180
DB 241 CTGCGGTTTATCTCCAGTGTGCTATCAATCGTTGCCAGCACTGGACAAAGGTCCTGCG 300

QY 1181 AGTCTCATAGCAGATACACTAGCAGCAACTCTCGAGTGTCTGAGGATGATGTAGATT 1240
DB 301 AGTCTCATAGCAGATACACTAGCAGCAACTCTCGAGTGTCTGAGGATGATGTAGACT 360

QY 1241 TTCACAGAGGCTGGAAACCAAGTCACTGGGGTGCACAGGAAGTACAGTACCTACA 1300
DB 361 TTCACAGAGGCTGGAAACCAAGTCACTGGGGTGCACAGGAAGTACAGTACCTACA 420

QY 1301 AGTTCGGTTGCGTGCCCAAGATTTTGCCTGGCGCATTTCTCTGCTGGAGTGGGAGCAC 1360

DB 421 AGTTGGGTCGCGGCAAGACTTTCGCGCGCATCTCTGTGGAGTCAGGAGGACAC 480
QY 1361 CGCCTCTTTCAGGTGCAAACTAGTTGAATTCGACCTTATCAACTGGGTG--GATTTTAA 1418
DB 481 CGCCTCTTTCAGGTGCAAACTAGTTGAATTCGACCTTATCAACTGGGTGATTTTAA 540
QY 1419 AGTTTGAATTAATCTCCATGAACAAGATGCAGAAAACATCGTTGTGATGTTGCCCAAG 1478
DB 541 AGTTTGAATTAATCTCCATGAACAAGATGCAGAAAACATCGTTGTGATGTTGCCCAAG 600
QY 1479 TGCATCGAATTTCTTTGGAGAGTATGATTAACAACATTTTATCTATCTTGAATGA 1538
DB 601 TGCATCGAATTTCTTTGGAGAGTATGATTAACAACATTTTATCTATCTTGAATGA 660
QY 1539 CGAGTGACCGTTCGTCACGTTGCTGTGTCAGTTA 1574
DB 661 CGAGTGACCGTTCGTCACGTTGCTGTGTCAGTTA 696

RESULT 3

CD001829/c

LOCUS

DEFINITION

3529_1.104_1_D01.X.1 3529 - 2 mm ear tissue from Schmidt and Hake

labs Zea mays cDNA, mRNA sequence.

CD001829

VERSION

CD001829.1 GI:30307156

KEYWORDS

EST.

Zeas mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 613)

AUTHORS

Walbot V.

TITLE

Maize ESTs from various cDNA libraries sequenced at Stanford

UNIVERSITY

Unpublished (1999)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 3529.1.104.1 row: D column: 01.

FEATURES

Location/Qualifiers

1..613

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="ear"

/dev_stage="2 mm"

/lab_host="E. coli XL0LR"

/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake

labs"

/note="Organ: ear; Vector: PAD-CAL4-2.1; Site 1: EcoRI;

Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu

amplified. Ampicillin is the selection marker."

ORIGIN

Query Match 36.5%; Score 597.2; DB 14; Length 613;

Best Local Similarity 99.3%; Pred. No. 6e-80;

Matches 610; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 825 AGTCACAGTATGCTGCTCGCTTGTAAATATGAGGAGGTATCTGTCAGTTGTTGAGGA 884

DB 613 AGTCACAGTATGCTGCTCGCTTGTAAATATGAGGAGGTATCTGTCAGTTGTTGAGGA 554

QY 885 CTTTGTGCTGATATCTGACCGTGCCTACACAAAGGCAAAATTTAGAAATGAAAAGTT 944

DB 553 CTTTGTGCTGATATCTGCGCTGCCCTACACAAAGGCAAAATTTAGAAATGAAAAGTT 494

AUTHORS Walbot, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1000174 row: E column: 12.
Location/Qualifiers
1. .589
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="dbEST:687075H12.x1"
/db_xref="taxon:4577"
/clone_lib="1000 - Unigene I from Maize Genome Project"
/note="This library represents the unique ESTs found in the first round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 486, 487, 496, 603, 605, 614, 618, 660, 683, 687, 707, and 945. Contigs were assembled using TIGR's CAP program and a representative EST from each contig was selected for the Unigene set. All singlets were also selected."

ORIGIN
Query Match 35.8%; Score 585.8; DB 12; Length 589;
Best Local Similarity 99.7%; Pred. No. 3.1e-78;
Matches 587; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 942 GTTGATTTCTGAACAGCTGCATGTCACATGCTCTTTCACACCTTATGCTTCATGAA 1001
ab 589 GTTGATTTCTGAACAGCTGCATGTCACATGCTCTTTCACACCTTATGCTTCATGAA 530
QY 1002 GAGTTTCTGAAGCTGCAGATGAGATGAACAGCTTGAGCTAGCTCATTTTTCATGCT 1061
Db 529 GAGTTTCTGAAGCTGCAGATGAGATGAACAGCTTGAGCTAGCTCATTTTTCATGCT 470
QY 1062 GGAGCTCTCTTGGTAGAATACCAATGCTGAATTTATCGGCTTCGCATCTGGCTGTCG 1121
Db 469 GGAGCTCTCTTGGTAGAATACCAATGCTGAATTTATCGGCTTCGCATCTGGCTGTCG 410
QY 1122 TCGGTTTATCTGCACAGTGTCTATCAATGCTTGGCAGCTGCAGAAAGTCTGCGA 1181
Db 409 TCGGTTTATCTGCACAGTGTCTATCAATGCTTGGCAGCTGCAGAAAGTCTGCGA 350
QY 1182 GTCTCATAGCAGATACACTAGCGACCAACTCTCGAGTGTCTCGAGGATGATGATGATTT 1241
Db 349 GTCTCATAGCAGATACACTAGCGACCAACTCTCGAGTGTCTCGAGGATGATGATGATTT 290
QY 1242 TCACGAGAGGCTGGNACCAAGTAAGTCACTGGCTGCAGAGGATACAGTACCTACAA 1301
Db 289 TCACGAGAGGCTGGNACCAAGTAAGTCACTGGCTGCAGAGGATACAGTACCTACAA 230
QY 1302 GTTCGGTTGCTGGCCCAAGATTTTGCTCGCAGATTCCTGCTGGAGTGGGAGGACACC 1361
Db 229 GTTCGGTTGCTGGCCCAAGATTTTGCTCGCAGATTCCTGCTGGAGTGGGAGGACACC 170
QY 1362 GCCTCCTTCAGGTGCAAACTAGTTGAATCGACTATTCGAATCGAGTGGGTGGAATTTTAAAGT 1421
Db 169 GCCTCCTTCAGGTGCAAACTAGTTGAATCGACTATTCGAATCGAGTGGGTGGAATTTTAAAGT 110
QY 1422 TTTTGAATCTCATGAACAGATCGAGAAACATCGTGTGATGTTGTCGCCAAAGTGC 1481
Db 109 TTTTGAATCTCATGAACAGATCGAGAAACATCGTGTGATGTTGTCGCCAAAGTGC 50
QY 1482 ATCGAATTTCTTGGAGAGTTATGATTAACAATTTTTTTTTTATCTATG 1530
Db 49 ATCGAATTTCTTGGAGAGTTATGATTAACAATTTTTTTTTTATCTATG 1

RESULT 6
LOCUS CD001830
DEFINITION 3529_1_104_1.D01.y.1 3529 - 2 mm ear tissue from Schmidt and Hake
labs Zea mays cDNA, mRNA sequence.
ACCESSION CD001830
VERSION CD001830.1 GI:30307157
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 579)
AUTHORS Walbot, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3529_1_104_1 row: D column: 01.
Location/Qualifiers
1. .579
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="ear"
/dev_stage="2 mm"
/lab_host="E. coli XL0LR"
/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
labs"
/notes="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI;
Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
amplified. Ampicillin is the selection marker."

ORIGIN
Query Match 35.4%; Score 579; DB 14; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.2e-77;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TCCTCCGTCCGTAAGCACCGCCGAGCGTCTCGGTGGATCAACAGGCGGCGGATCCG 69
Db 1 TCCTCCGTCCGTAAGCACCGCCGAGCGTCTCGGTGGATCAACAGGCGGCGGATCCG 60
QY 70 TCCTTCTTCCCTCTCTCTCGGGTTCGGGATCATGGCGGCGGCGGCTGAC 129
Db 61 TCCTTCTTCCCTCTCTCTCGGGTTCGGGATCATGGCGGCGGCGGCTGAC 120
QY 130 GAGAACAGGAGACCGGGGAGAGCCCGCCAGGCGTCCGAGACATGGCGAGCCG 189
Db 121 GAGAACAGGAGACCGGGGAGAGCCCGCCAGGCGTCCGAGACATGGCGAGCCG 180
QY 190 CGGCGCTCACGACATCAAGAACCTCTGTCGGGCTGCCCGTACCCCTACGCGCTGCC 249
Db 181 CGGCGCTCACGACATCAAGAACCTCTGTCGGGCTGCCCGTACCCCTACGCGCTGCC 240
QY 250 AAGAGCCCATGTGCAGAGAGCAAAAGGAGCAAAAGCAGCCAGCGTTGGCAAGCAGC 309
Db 241 AAGAGCCCATGTGCAGAGAGCAAAAGGAGCAAAAGCAGCCAGCGTTGGCAAGCAGC 300
QY 310 CGGCCCATGACAGGAATTCGCGCTCTTCGCGAGCAAGGCCAACTGTAATGTGAC 369
Db 301 CGGCCCATGACAGGAATTCGCGCTCTTCGCGAGCAAGGCCAACTGTAATGTGAC 360
QY 370 CCGATCGTAGCTGATCCAGAACCCGAGTTGTCAACAGAGGAATCAGTAGCGGATGCC 429


```

Db 361 CCGATGCTAGTCTGATCCAGAACCCGGAAGTTTGTCAACAGAGGAATCAGTAGGCGATGCC 420
Qy 430 ACCGTTGATATTGACGTGGAACTCTACGAGCTGGTTCGACGGTAGTGATAGTGAACATCGAC 489
Db 421 ACCGTTGATATTGACGTGGAACTCTACGAGCTGGTTCGACGGTAGTGATAGTGAACATCGAC 480
Qy 490 ATGGGTGCGACAGACAGAACAGGACATTATGAACGAAGATGAATTGCTCATGGATATTGAC 549
Db 481 ATGGGTGCGACAGACAGAACAGGACATTATGAACGAAGATGAATTGCTCATGGATATTGAC 540
Qy 550 AGTGCAGACTCGGGGACCCGCTTGTCTGCAACAGAAATAT 588
Db 541 AGTGCAGACTCGGGGACCCGCTTGTCTGCAACAGAAATAT 579

RESULT 7
CA249171
LOCUS SCSEBFL1107F08.9 FL1 Saccharum officinarum cDNA clone SCSBFL1107F08
DEFINITION 5', mRNA sequence.
ACCESSION CA249171
VERSION CA249171.1 GI:353331564
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 674)
Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 107 row: F column: 08
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..674
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSEBFL1107F08"
/lab_host="DH10B"
/clone_lib="Fl1"
/notes="Organ: Inflorescence at beginning of development
(lcm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
An unidirectional cDNA library generated from
[Inflorescence at beginning of development (lcm-long)].
cDNA was prepared from polyA+ mRNA using Superscript
Plasmid System kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

Query Match 34.9%; Score 570.2; DB 14; Length 674;
Best Local Similarity 31.1%; Pred. No. 6.3e-76;
Matches 614; Conservative 0; Mismatches 58; Indels 2; Gaps 1;

Qy 881 AGGACCTTGCTGATATCTGACCGCTTACACAAAGGGCAAAATTTAGAAATGAAA 940
Db 1 AGGACCTTGCTGATTTCTGATCGTCTTACACAAAGGGCAAAATTTAGAAATGAAA 60

```

```

Qy 941 AGTTGATTTCTGACACGCTCGAGTTCAACATGTTCTGTTCCAAACACCTTATGTCTTCATGA 1000
Db 61 AGTTGATTTCTGACACGCTCGAGTTCAACATGTTCTGTTCCAAACACCTTATGTCTTCATGA 120
Qy 1001 AGAGGTTTCTGAAAGCTTCAGATGCGAGATAAAGCAGCTGTAGCTAGCGTCAATTTTCAAGC 1060
Db 121 AGAGGTTTCTGAAAGCTTCAGATGCGAGATAAAGCAGCTGTAGCTAGCTAGCTCAATTTTCAAGC 180
Qy 1061 TGGAGCTTCTGTTGGTAGAATACCAATGCTGAATATATCGCCCTTCGATCTGGCTGCTG 1120
Db 181 TGGAGCTTCTGTTGGTAGAATATCAAAATGCTGAATATATCAGCCTTCGATCTGGCTGCTG 240
Qy 1121 CTGCGGTTTATATCTGACAGTGTGCTATCAATCGTTGCCAGCAGCTGACAAAAGTCTGCG 1180
Db 241 CTGCGGTTTATATCTGACAAATGTGCTATTAAATCGTTGCCCTCACTGACAAAAGTCTGCG 300
Qy 1181 AGTCTCATAGCAGATACACTAGCAGCAACTCTGCGAGTCTCGAGGATGATGCTAGATT 1240
Db 301 AGTCAATAGCAGATACACTAGCAGCAACTCTGCGAGTCTCGAGGATGATGCTAGATT 360
Qy 1241 TTCAACAGAGCTTGGAAACCAAGTAAGCTCACTGCGTGCACAGAACTCAGTACCTTACA 1300
Db 361 TTCAACAGAGCTTGGAACTGGCAAGCTCACTGCGTGCACAGAACTCAGTACCTTACA 420
Qy 1301 AGTTCGGTTCGTCGCGCAAGATTTTCTGCGAGTCTCTGCGAGTCTCTGCGAGTTCGGAGGACAC 1360
Db 421 AGTTCGGTTCGTCGCGCGCAAGACTTTGCGCGAGTCTCTGCGAGTTCGGAGGAGGACAC 480
Qy 1361 CGCTCTCTTCAAGTGCACAACTAGTTGAATCGACCTATTCAACTGGGTG--GATTTTTTAA 1418
Db 481 CGCTCTCTTCAAGTGCACATCTAGTTGAATCGACCTATTCAACTGGGTGTTGTTTATTTA 540
Qy 1419 AGTTTTAGATATCTCCATGAAAGATGCAAGATGCAAGAAACATGTTGATGTGCTGCGCAAAAG 1478
Db 541 AAGTNTTAGCATCTCTCGTGAACAGATGCAAGAAACATGTTGATGTGCTGCGCAAAAG 600
Qy 1479 TGCATCGAATTTCTTGGAGAGTTATGATTAACAACTTTTTTTTATCTATGTTGAATGA 1538
Db 601 TGCATCGAATTTCTTGGAGAGTTATGATTAACAACTTTTTTTTATCTATGTTGAATGA 660
Qy 1539 CGAGTACGCTCGG 1552
Db 661 CGAGTACGCTCGG 674

RESULT 8
CA122466
LOCUS SCULLR1033H06.g LR1 Saccharum officinarum cDNA clone SCULLR1033H06
DEFINITION 5', mRNA sequence.
ACCESSION CA122466
VERSION CA122466.1 GI:34975774
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 663)
Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 033 row: H column: 06

```

Seq primer: T7 Promoter Primer.

FEATURES
source

1. 663
Location/Qualifiers
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCULR1033H06"
/lab_host="DH10B"
/clone_lib="LRI"
/note="Organ: Leaf roll from field grown adult plants (large insert library); Vector: pSport1; Site 1: Sali; Site 2: NoRI; An unidirectional cDNA library generated from [leaf roll from field grown adult plants (large insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-column and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucrest.lad.ic.unimelb.br/public>"

ORIGIN

Query Match 33.7%; Score 552; DB 13; Length 663;
Best Local Similarity 92.5%; Pred. No. 3.4e-73;
Matches 613; Conservative 0; Mismatches 46; Indels 4; Gaps 3;

QY 865 TCTGTTCCAGTGTGTGAGACCTTGTGCTGTATATCTGACGCTGCTACACAAAGGGCAA 924
DB 2 TCAGTTCAGTGTGTGAGACCTTGTGCTGTATATCTGACGCTGCTACACAAAGGGCAA 61

QY 925 ATTTAGAAATGGAAAGTGTGATCTGAAACGCTGCGAGTTCACACATGTCTGTTCACAA 984
DB 62 ATTTAGAAATGGAAAGTGTGATCTGAAACGCTGCGAGTTCACACATGTCTGTTCACAA 121

QY 985 CCTATGTCCTCATGAAGAGTGTCTGAAAGCTGAGATGAGATGAGATGAGATGAGATG 1044
DB 122 CCTATGTCCTCATGAAGAGTGTCTGAAAGCTGAGATGAGATGAGATGAGATGAGATG 181

QY 1045 GCGTCATTTTCATGCTGGAGCTCTGCTGTGTAAGTACCAATGCTGAATTCGCGCCT 1104
DB 182 GTGTGATTTTCATGCTGGAGCTCTGCTGTGTAAGTACCAATGCTGAATTCGCGCCT 241

QY 1105 TCGCATCTGGCTGCTGGAGTGTATGCTGCAAGTGTGCTATCAATTCGTTGCCAGCAC 1164
DB 242 TCGCATCTGGCTGCTGGAGTGTATGCTGCAAGTGTGCTATCAATTCGTTGCCAGCAC 301

QY 1165 TGGACAAAGGCTGCGAGTCTCATAGCAGATACACTAGCACCACTGCTGGAGTGTCTG 1224
DB 302 TGGACAAAGGCTTGGAGTCTCATAGCAGATACACTAGCACCACTGCTGGAGTGTCTG 361

QY 1225 AGGATGATGGTAGATTTTCCACAGAGGCTGGAAACCAAGTCACTGGCGTGCACAGG 1284
DB 362 AGGATGATGGTAGATTTTCCACAGAGGCTGGAAACCAAGTCACTGGCGTGCACAGG 421

QY 1285 AAGTACGACTACTCAAGTTCGGTTCGGTGGCCAGATTTTGGCTGGCGAGTTCCTGCTG 1344
DB 422 AAGTACGACTACTCAAGTTCGGTTCGGTGGCCAGATTTTGGCTGGCGAGTTCCTGCTG 481

QY 1345 GAGTCGGAGGAGACACCGCTCTCTTCAGGTGCAATCTAGTTGAATGCACTTATT - CAAC 1402
DB 482 GAGTCGGAGGAGACACCGCTCTCTTCAGGTGCAATCTAGTTGAATGCACTTATT - CAAC 541

QY 1403 TGGGTGGATTTTAAAGTTCCTGAGTTCCTGAGTTCCTGAGTTCCTGAGTTCCTGAGT 1462
DB 542 TGGGTGGATTTTAAAGTTCCTGAGTTCCTGAGTTCCTGAGTTCCTGAGTTCCTGAGT 600

QY 1463 TGATGTCGCCAAAAGTCATGATTTCTTTTGGAGAGTTCATGATTAACAACTTTTTCCT 1522
DB 601 GATGTCGCCAAAAGTCATGATTTCTTTTGGAGAGTTCATGATTAACAACTTTTTCCT 659

QY 1523 TAT 1525
DB 660 TTT 662

RESULT 9
AI770352
LOCUS
DEFINITION
mays cDNA, mRNA sequence.
AI770352
VERSION
AI770352.1 GI:5268388
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 586)
AUTHORS
Walbot V.
TITLE
Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL
Unpublished (1999)
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 60661 row: D column: 02.

FEATURES
source

1. 586
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/tissue_type="mixed"
/dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
/clone_lib="606 - Ear tissue cDNA library from Schmidt
lab"
/note="Organ: immature ear; Vector: pBK-CMV; Site 1:
EcoRI; Site 2: XhoI; Mixed ear tissue cDNA library from
Schmidt lab"

ORIGIN

Query Match 32.5%; Score 531.6; DB 9; Length 586;
Best Local Similarity 94.2%; Pred. No. 4e-70;
Matches 552; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 553 GCAGACTCGGGAAACCCGCTTCTGCGACAGAGATATGTTAAAGAGCTTTACACCTTTTAC 612
DB 1 GCAGACTCGGGAAACCCGCTTCTGCGACAGAGATATGTTAAAGAGCTTTTACAGTTTAC 60

QY 613 AGAGAAAATGAGCGCTAAGAGTGTGTAAAGCCAGATTACATCTCCAGCCAAACAAGACATA 672
DB 61 AGAGAAAATGAGCGCTAAGAGTGTGTAAACCCCTGATTACATCTCCAGTCAGCAAGATA 120

QY 673 AACTCAAGATGAGAGCAATTCCTGATGCTGGCTGATTGAGTTCACTCAAGTTTGA 732
DB 121 AATCAAGATGAGAGCAATTCCTGATGCTGGCTGATTGAGTTCACTCAAGTTTGA 180

QY 733 CTGATGGATGAGACGCTCTTCTTATGTTAAACATAATAGATAGATTCTTGGAAAAGGAA 792
DB 181 CTGATGGAGAGAGCGCTATTTCTACGGTAAACGTAATAGATAGATTCTTGGAAAAGGAA 240

QY 793 GTGGTTCCAAAGGAAGAGCTACAACTGGTTGAGGACACAGCTATGCTGCTCGCTTGTAAA 852
DB 241 GTGGTTCCAAAGGAAGAGCTACAACTGGTTGAGGACACAGCTATGCTGCTCGCTTGTAAA 300

QY 853 TATGAGAGGATCTGTTCCAGTGTGTGAGGACCTTGTGCTGATATCTGACCGTCCCTAC 912
DB 301 TATGAGAGGATCTGTTCCAGTGTGTGAGGACCTTGTGCTGATATCTGACCGTCCCTAC 360

QY 913 ACAAAAGGGCAAAATTTTAGAAAAGGAAAGTTGATTCTTGAAACACGCTGCGATTCACATG 972

```

Db      361  ACAAAGGCAATCTAGAAATGGAAGTTGATCTGAACAGCTGCAATCAACATG 420
Qy      973  TCTGTTCCACACCTTATGCTTCATGAAGAGGTTTCTGAAGCTGCAGATCCAGATAAA 1032
Db      421  TCTGTTCCACACCTTATGCTTCATGAAGAGGTTTCTGAAGCTGCAGATCCAGATAAA 480
Qy      1033  CAGCTTGAGCTAGCGTCATTTTCATGCTGGAGCTCTGCTTGGTAGAAATACCAATGCTG 1092
Db      481  CAGCTTGAGCTAGCGTCATTTTCATGCTGGAGCTCTGCTTGGTAGAAATACCAATGCTG 540
Qy      1093  AATTATCGGCTTGGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1138
Db      541  AATTATAGGCTTCAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586

```

```

RESULT 10
CA122563/c
LOCUS      742 bp mRNA linear EST 23-SEP-2003
DEFINITION Saccharum officinarum cDNA clone SCULLR1033H06
            3', mRNA sequence.
ACCESSION CA122563
VERSION    CA122563.1 GI:34975871
KEYWORDS   EST.
SOURCE     Saccharum officinarum
ORGANISM   Saccharum officinarum

```

```

REFERENCE
AUTHORS    Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE      The libraries that made SUCEST
JOURNAL    Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT    Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 033 row: H column: 06
            Seq primer: SP6 Promoter primer.
            Location/Qualifiers

```

```

FEATURES             source
1..742
     /organism="Saccharum officinarum"
     /mol_type="mRNA"
     /db_xref="taxon:4547"
     /clone="SCULLR1033H06"
     /lab_host="DH10B"
     /clone_lib="LR1"
     /notes="Organ: Leaf roll from field grown adult plants
     (large insert library); Vector: pSPORT1; site 1: SalI;
     Site 2: NotI; An unidirectional cDNA library generated
     from leaf roll from field grown adult plants (large
     insert library). cDNA was prepared from polyA+ mRNA
     using SuperScript Plasmid System Kit (Invitrogen). The
     double-strand cDNAs were fractionated in a sepharose
     CL-2B 40cm-columns and fragments sizing between 0.8 and
     1.5 Kb were directionally cloned into the vector. Details
     of each source of RNA and library construction can be
     obtained at http://sucest.lad.ic.unicamp.br/public"

```

```

ORIGIN
Query Match      31.3%; Score 512.6; DB 13; Length 742;
Best Local Similarity 89.4%; Pred. No. 2.5e-67;
Matches 613; Conservative 0; Mismatches 55; Indels 18; Gaps 5;

Qy      925  ATTTAGAAATGGAAGTTGATCTGAACAGCTGCAGTTCACATGCTGTTGCAACA 984
Db      742  ATCTAAGAAATGGAAGTTGATTTTGAACACGTTGCATTCACATGCTGTTCCNACA 683

```

```

Qy      985  CCTATGCTTTCATGAAGAGTTTCTGAAGCTGCAGATGAACAGCTTGAGCTA 1044
Db      682  CCTATGCTTTCATGAAGAGTTTCTGAAGCTGCAGATGAACAGCTTGAGCAA 623
Qy      1045  GCGTCA-TTTTTCATGCTGAGCTCTGCTTGGTAGAATA-CCAAATGCTGAATATCGCG 1102
Db      622  GTGTCATTTTTCATGCTGAGCTCTGCTTGGTAGAATAATCAAAATGCTGAATATCAGC 563
Qy      1103  C-TTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
Db      562  CTTTGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503
Qy      1162  CACTGGACAAGCTCTGCGAGTCTCATAGCAGATACACTAGCGCAACCACTCCCTGGAGTGC 1221
Db      502  CACTGGACAAGGTTTGGAGTCACTAGCAGATACATTAGCCGCGACTCTCTGGAGTGC 443
Qy      1222  TCGAGGATGATGTTAGATTTTTCACGAGAGGCTGGAAACCAAGTCACTGCGGTGCAC 1281
Db      442  TCGAGGATGATGTTAGACTTTTTCACGAGAGGCTGGAACTGGCAAGCTCACTGCGGTGCAC 383
Qy      1282  AGGAAGTACAGTACCTACAAAGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1341
Db      382  AGGAAGTACAGTACCTACAAAGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 323
Qy      1342  CTGAGTCTGGGAGGACACCGCTCTCTTCAAGTGCRAAATAGTTGAATCGACCTATTCAA 1401
Db      322  CTGAGTCTGGGAGGACACCGCTCTCTTCAAGTGCRAAATAGTTGAATCGACCTATTCAA 263
Qy      1402  CTG-----GTGGATTTTAAAGTTTGTAGAACTCCATGACACAGATCGAAGAACAT 1457
Db      262  CTGGGTGGTGGATTTTAAAGTTTGTAGAACTCCATGACACAGATCGAAGAACAT 203
Qy      1458  CGTGTGATGTTGCCAAAGTGCATCGAATTTCTTTGGAGAGTTATGATTAAACAATTT 1517
Db      202  CGTGTGATGTTGCCAAAGTGCATCGAATTTCTTTGGAGAGTTATGATTAACTGTTT 143
Qy      1518  TTTTATCTATGTTGAATGACGAGTGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1577
Db      142  TTTTATCTATGTTGAATGACGAGTGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 94
Qy      1578  TGGCGCTAATAACAAACTGTCCAGTT 1603
Db      93  TGGCGCTAATAACGACTGTCTGTT 68

```

```

RESULT 11
CA223571/c
LOCUS      683 bp mRNA linear EST 25-SEP-2003
DEFINITION SCJFFL1C03E09, b FL1 Saccharum officinarum cDNA clone SCJFFL1C03E09
            3', mRNA sequence.
ACCESSION CA223571
VERSION    CA223571.1 GI:35280031
KEYWORDS   EST.
SOURCE     Saccharum officinarum
ORGANISM   Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 683)
AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE     The libraries that made SUCEST
JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT   Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br

```

Plate: C03 row: E column: 09
Seq primer: SP6 Promoter primer.
Location/Qualifiers
1..683
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJFFL1C03E09"
/lab_host="DH10B"
/clone_lib="Fli1"
/note="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [inflorescence at beginning of development (1cm-long)] cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>"

CG453107
LOCUS
DEFINITION
CG453107
ACCESSION
CG453107
VERSION
CG453107.1
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 778)
AUTHORS
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
CONSORTIUM for Maize Genomics
Unpublished (2002)
JOURNAL
COMMENT
Other_GSSs: OGVGS27TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..778
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0478F05"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBGSK; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

Query Match 30.7%; Score 502.4; DB 14; Length 683;
Best Local Similarity 91.2%; Pred. No. 8.9e-66;
Matches 560; Conservative 0; Mismatches 41; Indels 13; Gaps 2;
QY 992 TCTTCATGAAGAGGTTCTGAAAGCTGCAGATGCAGATAAACAGCTTGAGCTAGCGTCAT 1051
Db TCTTCATGAAGAGGTTCTGAAAGTTGCAGATGCAGATAAACAGCTTGAGCTAGTCAT 624
QY 1052 TTTTCATCTGGAGCTCTGCTGTAGTAATACCAATGCTGAATATCGGCTTCGCATC 1111
Db TTTTCATCTGGAGCTCTGCTGTGTAGTAATACCAATGCTGAATATCGGCTTCGCATC 564
QY 1112 TGGCTGCTGCTGCGGTTTATCTACTGCACAGTGTGCTATCAATCGTTCGACACTGGACAA 1171
Db TGGCTGCTGCTGCGGTTTATCTACTGCACAAATGCTATTAATCGTTCGCTCAGTGGACAA 504
QY 1172 AGTCTGGAGTCTCATAGCAGATACACTAGGACCAACTCTGGAGTCTCGAGGATGA 1231
Db AGTCTGGAGTCTCATAGCAGATACACTAGGACCAACTCTGGAGTCTCGAGGATGA 444
QY 1232 TGGTAGATTTTCCACAGAAAGGCTGGAACAGTCAAGCTCACTGGGCTGCACAGGAAGTACA 1291
Db TGGTAGATTTTCCACAGAAAGGCTGGAACAGTCAAGCTCACTGGGCTGCACAGGAAGTACA 384
QY 1292 GTACCTACAAGTTCCGTTGCGTGCCAAAGATTTTCCCTGCGCAGATTCCTGCTGAGTCGG 1351
Db GTACCTACAAGTTCCGTTGCGTGCCAAAGATTTTCCCTGCGCAGATTCCTGCTGAGTCAG 324
QY 1352 GAGGACACCGGCTCCTTCAGTGCACAACTAGTTGAATCGACCTATTCAACTGGGTG -G 1409
Db GAGGACACCGGCTCCTTCAGTGCACAACTAGTTGAATCGACCTATTCAACTGGGTG 264
QY 1410 ATTTTAAAGTTTAAAGTACTCCATGAACAAGATCGAAGAAACATCGTTGTTGATGTT 1469
Db ATTTTAAAGTTTAAAGTACTCCGTTGAACAAGATCGAAGAAACATCGTTGTTGATGTT 204
QY 1470 GCCCAAGAGTGCATCGAATTTCTTTGGAGAGTTATGATTACAACTTTTATATCTAT 1529
Db GCCCAAGAGTGCATCGAATTTCTTTGGAGAGTTATGATTACAACTTTTATATCTAT 144
QY 1530 GTTGAATGACGAGTGCAGGTCGGTGCACGTTGCTGTTGTGTCAGTTTATCTGCGGTAATAA 1589
Db GTTGAATGACGAGTGCAGGTCGGTGCACGTTGCTGTTGTGTCAGTTTATCTGCGGTAATAA 95
QY 1590 CAAACTGTCAGTT 1603
Db CAAACTGTCAGTT 81
RESULT 12

Query Match 29.7%; Score 485.2; DB 29; Length 778;
Best Local Similarity 86.4%; Pred. No. 3.1e-63;
Matches 584; Conservative 0; Mismatches 5; Indels 87; Gaps 1;
QY 1033 CAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAATACCAATGCTG 1092
Db CAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAATACCAATGCTG 87
QY 1093 AATTATCGGCTTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1152
Db AATTATCGGCTTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 147
QY 1153 CGTTGCCAGCAGCTGGACAAAGGCTTGGAGTCTCATAGCAGATACACTAGCAGCAACTC 1212
Db CGTTGCCAGCAGCTGGACAAAGGCTTGGAGTCTCATAGCAGATACACTAGCAGCAACTC 207
QY 1213 CT----- 1214
Db CTGTAAGTCCATTTCAAGTCAGTCTCTCACTGATTAAGTATCTTTATGCTGACTTT 267
QY 1215 -----GGAGTCTCGAGGATCATGTTAGATTTTCAC 1245
Db CTGTGTGTACCTTTTGTCTTCTCACCAGGAGTCTCGAGGATGATGTTAGATTTTCAC 327
QY 1246 CAGAAGGCTGGAACCAAGTAAAGTCTGCTGCGGTCGACAGGAAGTACAGTCTTACAGTTTC 1305
Db CAGAAGGCTGGAACCAAGTAAAGTCTGCTGCGGTCGACAGGAAGTACAGTCTTACAGTTTC 387
QY 1306 GGTTCGCTGCCAGATTTTTCGCTGCGCAGTTCCCTGCTGGAGTCCGGAGGACACCGCT 1365
Db GGTTCGCTGCCAGATTTTTCGCTGCGCAGTTCCCTGCTGGAGTCCGGAGGACACCGCT 447
QY 1366 CTTTCAGGTGCAAACTAGTGAATGACCTATTCAACTGGGTGGGATTTTAAAGTTTT 1425

```

Db      448 CCTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTGGATTTTAAAGTTTTT 507
QY      1426 AGAATACCTCATGACACAGATCGAGAAACATCGTGTGTGATGTTGCCCAAAAGTCATCG 1485
Db      508 AGAATACCTCATGACACAGATCGAGAAACATCGTGTGTGATGTTGCCCAAAAGTCATCG 567
QY      1486 AATTCTTTGGAGAGTATGATTAAACAACTTTTTTTTATCTATGTTGAATGACAGATGA 1545
Db      568 AATTCTTTGGAGAGTATGATTAAACAACTTTTTTTTATCTATGTTGAATGACAGATGA 627
QY      1546 CGGTGGTCACTGTGTGCTTGTGCGATTAATCTGCGGCTAATAACAACTGTCCAGTTNT 1605
Db      628 CGGTGGTCACTGTGTGCTTGTGCGATTAATCTGCGGCTAATAACAACTGTCCAGTTAT 687
QY      1606 TCTNAAAAAATAAAAA 1621
Db      688 TCTAAAAAACACAGAA 703

RESULT 13
LOCUS   CG453099/c
DEFINITION
CG453099 779 bp DNA linear GSS 17-SEP-2003
genomic survey sequence.
ACCESSION
CG453099
VERSION
CG453099.1 GI:34838099
KEYWORDS
SOURCE
GSS.
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 779)
REFERENCE
1 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.,
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGVGS27TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..779
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZM0.7.1.5 KB"
/notes="Vector: pBCSK-; Site: 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 29.7%; Score 485.2; DB 29; Length 779;
Best Local Similarity 86.4%; Pred. No. 3.1e-63;
Matches 584; Conservative 0; Mismatches 5; Indels 87; Gaps 1;
QY 1033 CAGCTTGAGCTAGCGTCATTTTCATCGTGGAGCTCTGCTGGTAGAATACCAAAATGCTG 1092
Db 751 CAGCTTGAGCTAGCGTCATTTTCATCGTGGAGCTCTGCTGGTAGAATACCAAAATGCTG 692
QY 1093 AATTATCGGCTTCGATCGTCTGCTGGGTTTATACGACAGTGTCTATCAAT 1152
Db 691 AATTATCGGCTTCGATCGTCTGCTGGGTTTATACGACAGTGTCTATCAAT 632
QY 1153 CGTTGCCAGCAGTGGCAAAAGTCTCGAGTCTCATAGCAGATACACTAGCGACCAATC 1212

```

```

Db      631 CGTTGCCAGCAGTGGCAAAAGTCTCGAGTCTCATGACAGATACACTAGCGACCAATC 572
QY      1213 CT----- 1214
Db      571 CTGTAAGTCCANTTCAAGTCAGTTCTCTACTGCTATGATGAAGCATCTTTTATGCTGACTTT 512
QY      1215 -----GGAGTGTCTCGAGATGATGCTAGATTTTTCAC 1245
Db      511 CTGTGTGTACCTTTTCTGCTTCTCACCAGGAGTGTCTCGAGGATGATGTTAGATTTTTCAC 452
QY      1246 CAGAAGGCTGGAAACCAAGTAAAGTCACTGGCGTGCAAGGAAGTACAGTACCTTAAAGTTTC 1305
Db      451 CAGAAGGCTGGAAACCAAGTAAAGTCACTGGCGTGCAAGGAAGTACAGTACCTTAAAGTTTC 392
QY      1306 GGTTCGTGGCCCAAGATTTTCTCTGCGCAGTTTCTCTGCGCAGTTCCTGCGAGTCCGAGAGGACACCGCT 1365
Db      391 GGTTCGTGGCCCAAGATTTTCTCTGCGCAGTTCCTGCGAGTCCGAGAGGACACCGCT 332
QY      1366 CCTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTGGATTTTAAAGTTT 1425
Db      331 CCTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTGGATTTTAAAGTTT 272
QY      1426 AGAATACCTCATGACACAGATCGAGAAACATCGTGTGATGTTGCCCAAAAGTGCATCG 1485
Db      271 AGAATACCTCATGACACAGATCGAGAAACATCGTGTGATGTTGCCCAAAAGTGCATCG 212
QY      1486 AATTCTTTGGAGAGTATGATTAAACAACTTTTTTTTATCTATGTTGAATGACAGTGA 1545
Db      211 AATTCTTTGGAGAGTATGATTAAACAACTTTTTTTTATCTATGTTGAATGACAGTGA 152
QY      1546 CGGTGGTCACTGTGTGCTTGTGCGATTAATCTGCGGCTAATAACAACTGTCCAGTTNT 1605
Db      151 CGGTGGTCACTGTGTGCTTGTGCGATTAATCTGCGGCTAATAACAACTGTCCAGTTAT 92
QY      1606 TCTNAAAAAATAAAAA 1621
Db      91 TCTAAAAAACACAGAA 76

RESULT 14
LOCUS   CG278953/c
DEFINITION
CG278953 873 bp DNA linear GSS 25-AUG-2003
genomic survey sequence.
ACCESSION
CG278953
VERSION
CG278953.1 GI:34192236
KEYWORDS
GSS.
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 873)
REFERENCE
1 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGVAT49TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..873
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"

```

```

FEATURES
source
Location/Qualifiers
1..873
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"

```


Db 479 AACCCTGTCAGCAACAGATATGTGAAGAGCTTTACAAGTTCTACAGAGAAATGAG 538
QY 625 GCTAAGAGTTGTCTAAGGCCAGATTACATGTCCAGCCCAACAAAGACATAAACTCAAAGATG 684
Db 539 GCTAAGAGTTGTGTGAAGGCCCTGATTACATGTCCAGTCAACAAAGATATAAACTCAAAGATG 598
QY 685 AGAGCAATTCTGATTGACTGGCTGATTG 712
Db 599 AGAGCGATTCTGATTGACTGGCTGATTG 626

Search completed: March 20, 2004, 23:04:32
Job time : 4453 secs